Human zil Human int Human int Human ext Human ext Human II-Processed Human II-Novel hum Human sec Novel hum Human sec Human sec Human sec Human sec Human sec Human sec Human sec

Aay70928 I Adh89068 I Adh89068 I Aab48081 I Aab48081 I Adh65905 I Aay96933 I Aay96933 I Aby96936 I Abu71576 I Abu71576 I Abu91202 K Abu9130 I Abu912546 H Abu91313 N Abu91313 N Abu91313 N Abu91313 N Abu91313 N Abu91313 N

Sequence:

Run on:

Searched:

```
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primate interleukin-1 like (IL-1-zeta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76. 80
/label= beta_strand_3
91. 96
/label= beta_strand_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .07. .113
/label=_beta_strand_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= beta_strand_6
131. .136
/label= beta_strand_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8. .64
label= beta_strand_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69. .74
/label= beta_strand_2
AAY70928
ADH89068
ADH89068
ABAB48081
ADL66905
ADL66905
AAY96933
AAY96933
AAY96933
AAY96933
ABU90946
ABU71276
ABU71276
ABU71276
ABU71576
                                                                                                                                                                                                                                                                                                                                                   ABU98333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY91884 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118. .126
 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2000
 1010
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
99610
90610
90610
90610
90610
90610
90610
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY91884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY91884
   Aay96940 Human IL-
Aab52266 Human int
Aab5136 Interleuk
Adn05012 Antipsori
Aay71084 Human zil
Aay7093 Human zil
Aay95299 Human zil
Aay95299 Human int
Aay91885 Primate i
Aab47186 IL-1 rela
Aab47186 Human int
Adn15868 Human int
Adn15868 Human int
Adn15868 Human int
Adn15869 Human int
Adn18979 Human zil
Aay96938 Human zil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aay91884 Primate i
Adj88304 Human int
Adl15866 Human int
Ado04677 Human int
Aay70927 Human int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human zil
Human lib-
Human int
Antipsori
Human zil
Human zil
Human zil
Human zil
Human zil
Human int
Primate i
IL-1 rela
Human int
Human int
                                                                                                                               September 29, 2005, 10:55:38; Search time 65.5 Seconds (without alignments) 1287.233 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                          US-10-695-195-2
1155
1 MSFVGENSGVKMGSEDWEKD.....IEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                            2105692
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY91884
ADJ88304
ADL1886304
ADC16866
ADO04677
AAY96920
AAB82136
AAB85136
AAR9529
AAY1084
AAY70933
ADH89075
AAX95299
AAX95299
AAX95299
AAX95299
AAX95299
AAX968116
AAX968116
AAX968116
AAX968106
ADL18866
ADG88306
ADG88306
ADG88306
ADG88306
ADG88306
ADG88306
AAX968306
                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Geneseq_16Dec04:*

1. geneseqp1980s:*
2. geneseqp1980s:*
3. geneseqp2001s:*
5. geneseqp2001s:*
6. geneseqp2003s:*
7. geneseqp2003bs:*
8. geneseqp2003bs:*
                                                                                                 using
                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                               - protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155
1130
1130
1130
11330
11130
11127
11127
11126
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                     OM protein
```

Database

100. .106 note= "forms a loop which is part of a primary binding segment to the IL-1 receptor type" Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever; hypoglycemia; plasma iron; plasma zinc; acute liver response; plasma copper. 176. .180 /label= beta\_strand\_10 .85. .204 |label= beta\_strand\_11 201. .204 /label= beta\_strand\_12 .63. .169 /label= beta\_strand\_9 WO200017363-A2 Domain Domain Domain Domain 

30-MAR-2000.

```
Beta strand domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta strand domain
                                                                                                                                                         'note = Beta strand domain
                                                                                                                                                                                                                     = Beta strand domain
                                                                                                                                                                                                                                                                                                        'note = Beta strand domain
                                                                                                                                                                                                                                                                                                                                                                                                              'note = Beta strand domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                          /note = Beta strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note = Beta strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139. .146
/note= "Epitope"
141. .152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Epitope"
156. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Epitope"
                    ). .20
'note= "Epitope"
                                                                                                                                                                                                "Epitope"
                                                                                                                                                                                                                                                                                                                                                          92. .103 /
/note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131. .136
/note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Epitope"
         'note= "Epitope"
                                                 "Epitope"
                                                                      "Epitope"
                                                                                          "Epitope"
                                                                                                               "Epitope"
                                                                                                                                   "Epitope"
                                                                                                                                                                            "Epitope"
                                                                                                                                                                                                                                         "Epitope"
                                                                                                                                                                                                                                                               "Epitope"
                                                                                                                                                                                                                                                                                   "Epitope"
                                                                                                                                                                                                                                                                                                                                                 "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163. .169
/note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175. .180
'note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                          'note= "Epitope'
                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note = Be
179. .190
                                                                                                                                                                                                       . .74
/note = .
.9
                                                                                                                                                                                                                                                                                                                                                                                                 .113
                                                                                                                                                                                                                                                                                                                                                                                                                                            .126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .169
                                                                                                                                                                                                                                                                                                                                                                                                                      .113
                                                                                                                                                                                                                                                                                                                                                                               .105
                                       .20
                                                                                                                         .60
                                                                                                                                                                                                                                                     .87
                                                                                                                                                                                                                                                                                            .80
                                                            .30
                                                                                                                                              .64
                                                                                  .41
                                                                                                                                                                   .64
                                                                                                                                                                                                                                                                          76. .81
                                                                                                                                                                                                                                                                                                                 96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                              /note=
                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                            /note=
                                                                                                                                                                                                                                                                                    /note=
                                                   'note=
                                                                                                               /note=
                                                                                                                                    /note=
                                                                       'note=
                                                                                                    Region
                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                               Domain
                                                                                                                                                                                        Region
                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                    Region
                                        Region
                                                             Region
                                                                                  Region
                                                                                                                          Region
                                                                                                                                                                    Region
                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
The present sequence is a primate interleukin-1 like molecule, designated II-1-zeta. An alternative sequence, encoded by an allelic variant is given in AAY91885. The 12 beta strands, indicated in the features table, fold into a beta-trefoil fold. The specification claims an isolated or recombinant polypeptide that: (a) specifically binds polyplonal antibodies generated against at least a 12 consecutive amino acid segment of IL-1-zeta (see AAY91884) or its allalic variant (see AAY91885); and of IL-1-zeta (see AAY91884) or its allalic variant (see AAY91885); and form AAY91904-06. The preferred 12 consecutive amino acid segment is chosen from AAY91907-18 or AAY91912-12. IL-1-zeta is likely to play a role in systemic inflammatory reactions, such as fever, hypoglycemia, reduced plasma copper. IL-1-zeta binding compounds (comprising antigen binding sheeps and IL-1-zeta polypeptides are also useful for both diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                         New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful for diagnostic and therapeutic purposes, comprises a 128 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-1zeta, gene therapy; immune system; haematopoietic cell; inflammatory disorder; infection; allergy; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1155; DB 3; Length 218; 100.0%; Pred. No. 9.3e-121; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                   Claim 1; Page 102; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-1zeta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ88304 standard; protein; 218
          99WO-US020868
                             98US-00156966
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 218; Conservative
                                                  (SCHE ) SCHERING CORP.
                                                                                          WPI; 2000-283588/24.
N-PSDB; AAA08512.
                                                                                                                                                                                                                                                                                                                                       therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                           Sequence 218 AA;
          17-SEP-1999;
                              18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                       Timans JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ88304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ88304
 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FXSXXXXXXXXXXXX
```

99US-00398412

```
Novel isolated or recombinant interleukin 1 zeta polypeptide useful as immmunogen for producing specific antibodies or for developing anti-
                                     antiinflammatory; interleukin 1 zeta; IL-1 zeta; immmunogen; antisera production; antibody production; anti-inflammatory; human.
            Human interleukin 1 zeta (IL-1zeta) seqid 2.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2; 42pp; English.
                                                                                                                                                                            27-OCT-2003; 2003US-00695195
                                                                                                                                                                                                                                                                                                                                                                                            inflammatory therapeutics.
                                                                                                                                                                                                                                                                                                               WPI; 2004-304623/28.
                                                                                                                                                                                                                                                    (TIMA/) TIMANS J C.
                                                                                                                                                                                                                                                                                                                                N-PSDB; ADL15865.
                                                                                                                   US2004068099-A1.
                                                                                                                                                                                                                         17-SEP-1999;
                                                                                       Homo sapiens
                                                                                                                                                                                                           8-SEP-1998;
                                                                                                                                              08-APR-2004
                                                                                                                                                                                                                                                                                     Timans JC;
쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated or recombinant nucleic acid encoding interleukin-1zeta polypeptide. The invention is useful in gene therapy. The composition and methods are useful in diagnosing or treating degenerative or abnormal conditions which directly or indirectly involve development, differentiation or function, e.g. of the immune system and/or haematopoietic cells. The invention may also be used for preventing or treating other diseases or disorders associated with abnormal expression or triggering of response to the interleukin, such as inflammatory disorders, infection, allergies or cancer. The present sequence is human interleukin-1zeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding mammalian interleukin-1 polypeptides, useful for diagnosing, preventing or treating diseases associated with abnormal expression of interleukin, e.g. inflammation, infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGBFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1155; DB 8; Length 218; 100.0%; Pred. No. 9.3e-121; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
   Beta strand domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 2; 36pp; English
                               "Epitope"
                                                             "Epitope"
                                                                                         "Epitope"
                                                                                                                                                                                                                99US-00398412
                                                                                                                                                                                                                                            98US-0100948P
               185. .190
/note= "Ep
193. .204
                                                                           .207
                                                                                                       .216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 218; Conservative
      note =
                                                                                       /note= '
                                                           /note= '201. .2(
                                                                                                                        /note=
                                                                                                                                                                                                                                                                          (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                     WPI; 2004-189656/18.
N-PSDB; ADJ88303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 218 AA;
                                                                                                                                                                                                                                             18-SEP-1998;
                                                                                                                                                    US6680380-B1
                                                                                                                                                                                                                 17-SEP-1999;
                                                                                                                                                                                20-JAN-2004
                                                                                                                                                                                                                                                                                                       Timans JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
                                              Region
                                                                            Region
                  Region
                                                                                                          Region
```

```
The invention describes an isolated or recombinant interleukin 1 zeta polypeptide (I) that specifically binds to polyclonal antibodies consecutive amino acid segment of two generated against at least a 12 consecutive amino acids segment of two fully defined sequences (S1) and (S2) having 218 amino acids as given in the specification and comprises at least one sequence chosen from (S1) and (S2). Also described are: a fuelon protein comprising (I) or its sequence or sequence of another cytokine or chemokine; a binding compound (II) an antigen binding site from an antibody, which specifically binds (II) an antigen binding site from an antibody, which specifically binds (II) an antigen binding site from an antibody which specifically binds (II), (I) or (II) and a carrier such as an aqueous compound e.g., water, call in copical or parental administration; an isolated for oral, rectal, can and or buffer, where the carrier is formulated for oral, rectal, consal, topical or parental administration; an isolated or recombinant (C) or (S2); a cell (IV) transformed with (III); a method of modulating a cell (IV) transformed with (III); a method of modulating a cell involved in an inflammatory response, by contacting the cell with an oral producing an antibody as mentioned for unserving a compartment of (II), (II) or an antigen: antibody complex. (I) is useful for developing more effective anti-inflammatory complexed or useful for developing more effective anti-inflammatory in the representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1155; DB 8; Length 218; 100.0%; Pred. No. 9.3e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zeta polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

Ė

ADL15866 standard; protein; 218

RESULT 3 ADL15866

Š 셤

용

δ 셤

ò 셤 ઠે (first entry)

01-JUL-2004

ADL15866;

SXXXX

```
Interleukin-1 zeta; inflammatory reaction; immune system; IL-1 zeta; immunological disorder; human.
                                                                                                                                                                                                                                                                                                                                                                                                                               note= "IL-1 receptor binding site B "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02. .204
note= "IL-1 receptor binding site A "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "IL-1 receptor binding site B "
                                                                                                                                                                                                     note= "IL-1 receptor binding site B"
                                                                                                                                                                                                                                                                                                                                                                                binding site C
                                                                                                                                                                                                                                                                                                  "IL-1 receptor binding site A
13. .56
note= "IL-1 receptor binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding site
                                                                                                                                                                                                                                                                                                                                 "IL-1 receptor binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                               binding site
                                                                                                                                                                                                                    binding
                                                                                                                                                                                                                                                   binding
                                                                                                                                                                                                                                                                                   'note= "IL-1 receptor binding
                                                                                                                                                                                                                                                                                                                                                                         27. .153
note= "IL-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81. .186
note= "IL-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                131. .136
/note = Beta7 strand
154. .161
/note = Beta8 strand
159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "IL-1 receptor
                                                                                                                                                                                                                                            72. .74
'note= "IL-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                "IL-1 receptor
                                                                                                                                                                                                                   "IL-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Betall strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betal2 strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Betal0 strand
                                                                                                                                                                                                                                                           76. .80
/note = Beta3 strand
                                                                                                                                                                                                                                                                                                                 /note = Beta4 strand
95. .103
                                                                                                                                                                                                                                                                                                                                                  Beta5 strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta9 strand
                                                                                                                                                                                                                                     = Beta2 strand
                                                                                                                                                                                                                                                                                                                                                                 Beta6 strand
                                                                                                                                                                                     /note = Betal strand
                                                                                                                                                     Location/Qualifiers
                                                 $
                                                 AD004677 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                       |61. .164
|note= "IL
|63. .169
                                                                                                                                                                                                                                                                                                                                                         118. .126
/note = Be
                                                                                                                                                                                                                                                                                                       .96
/note = <sup>r</sup>
5.
                                                                                                                                                                                                                                                                                                                                  /note= "IL
107. .113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .76. .180
'note = Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185. .204
'note = Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01. .204
note = Be
                                                                                                Human interleukin-1 zeta.
                                                                                                                                                                                                                                                                                          .87
                                                                                                                                                                              . 64
                                                                                                                                                                                                              99.
                                                                                                                                                                                                                                                                                                                                                  note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                               note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
207
                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                     note
                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                             Binding-site
                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                       sapiens
                                                                               29-JUL-2004
                                                                 AD004677;
          181
                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                             Domain
                                                                                                                                       Ношо
                                 RESULT
                                                                 g
```

site A

ф

ø

site

Ø

site B "

Ā

m

```
ö
                                                                                                                                                                                                                                                                              New isolated or recombinant interleukin-1 zeta polypeptide and related reagents such as antibodies, useful for treating inflammatory disease and as probes for diagnosing immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to interleukin-1 zeta polypeptide and polymucleotide. The agonist or antagonist of the interleukin-1 zeta is belymucleotide. The agonist or antagonist of the interleukin-1 zeta is useful in modulating a cell that is involved in inflammatory response. The peptide fragments of IL-1 zeta are useful in research and diagnostic tools in the study of inflammatory reactions to antigenic challenge and the development of more effective anti-inflammatory therapeutics. Interleukin-1 zeta is useful in regulation and/or development of immune system. A polymucleotide encoding IL-1 zeta is useful for detecting the expression level of the polypeptide in a patient suspected of having an immunological disorder. The present sequence is human interleukin-1 zeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis; psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer; anaemia; inflammatory bowel disease; acute neuropathology; shock; chronic neuropathology; respiratory disease syndrome; restenosis; acquired immune deficiency syndrome; ALDS; antiinflammatory; cytostatic; anti-arthritic; anti-psoriatic; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCDKDKGGSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1155; DB 8; 100.0%; Pred. No. 9.3e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70927 standard; protein; 218 AA
                                                                    27-OCT-2003; 2003US-00694978
                                                                                                     98US-0100948P
                                                                                                                                                                                                                               WPI; 2004-374758/35.
N-PSDB; ADO04676, ADO04691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human zilla4 protein.
                                                                                                                                                         (TIMA/) TIMANS J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 218 AA;
US2004087766-A1
                                                                                                       18-SEP-1998;
                                                                                                                          17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2000
                                   06-MAY-2004
                                                                                                                                                                                              Timans JC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
(ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                              WO200024899-A2
                                                                                                                                                                        27-OCT-1999;
                                                                                                                                                                             27-OCT-1998;
       Homo sapiens
                                                                                                                                                                   04-MAY-2000
                                                                                                                                          Domain
                                                                                                                                               Domain
                                                                                                                                                      Domain
            Key
Domain
                                                                                                                 Domain
                                                                                                                      Domain
                                                                                                                             Domain
                                                                                                                                  Domain
                                                                                        Domain
                                                                                                     Domain
                                                                                                          Domain
                   Domain
                          Comain
                               Domain
                                       Domain
                                            Domain
                                                   Domain
                                                        Domain
                                                                Domain
                                                                     Domain
                                                                            Domain
                                                                                 Domain
                                                                                             Domain
```

```
The present sequence is the human interleukin (IL)-1 homolog zilla4 protein. This protein contains a core structure of 12 betea strands wound into a beta-barrel, with the beta-strands seperated from each other by loops. The loops between these beta-strands are highly variable among the family members and are believed to be involved in receptor binding. The zilla4 proteins modulate inflammation and other immunological processes and are therefore useful for treatment of arthritis, psoriasis, septic shock, graft-versus-host disease and leukaemia. Other diseases that may be modulated by zilla4 proteins include cancer, anaemia, inflammatory bowel disease, acute and chronic neuropathologies, shock, respiratory disease syndrome, restenosis and acquired immune deficiency syndrome
                                                                                       Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
disease, leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hIL-IRalV; human interleukin-1 receptor antagonist-1; IL-11p; osteopathic; interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic; anti-arthritic; antimicrobial; respiratory; vaccine; anti-ischemic; dermatalogical; immunomodulatory; gastrointestinal;
                                                                                                                                                                                            sequence is the human interleukin (IL)-1 homolog zilla4
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1130; DB 3; Length 218;
Pred. No. 6e-118;
1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IL-1 receptor antagonist 1 V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96940 standard; protein; 218 AA
              2
                                                                                                                                                                 Claim 4; Fig 2; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0113430P.
99US-0116843P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US030720
                                                                                                                                                                                                                                                                                                                                                                                                                                           97.8%;
98.2%;
               Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.2
Matches 214; Conservative
              West RR, Sheppard PO,
                                               WPI; 2000-350740/30
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 218 AA;
                                                                 N-PSDB; AAD00210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200039297-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1998;
22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Beta_strand
70. .174
note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32. .138
|Tabel= Beta_strand
139. .153
|note= "Variable loop region involved in receptor

    164
    note= "Variable loop region involved in receptor

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90. .200
note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24. .131 -
note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80. .186 -
note= "Variable loop region involved in receptor
                                                                                                                                                        'note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                          "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                             "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                               note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14. .117 -
note= "Variable loop region involved in
     anti-anaemic; neuroprotective; vasotropic; anti-human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                               //. .79
/label= Beta_strand
80..89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201. .204
/label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75. .179
label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87. .189
label= Beta_strand
                                                                                                                      /label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                   'label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                   08. .<u>I</u>13
label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18. .123
label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta_strand
                                                                                                                                                                                                        label= Beta_strand
                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US025038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154. .160
/label= Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .169
                                                                                                                                                                                                                                                                                                                                                                                               .107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'nding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inding"
                                                                                                                                                                                                                                                                                                                                                 binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inding"
                                                                                                                                                                          binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "inding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inding"
                                                                                                                                                                                                                            . 76
                                                                                                                                                                                                                                                             binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                      inding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inding"
                                                                                                                                                                                                                                               note=
```

ö

Gaps

ö

9 9 120

```
WO200063226-A1
   Homo sapiens
                                                                                                                   16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001
                                                         26-OCT-2000
                                                                                                                                                                          PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB85136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                             Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB85136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                 polypeptide (IL-IIp) that metains one or more activities of the peptide from which it is derived, such as the IL-IRR binding activity of a human interleukin-1 receptor antagonist-1 (IL-IRB) binding activity of a human uncleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for recombinantly producing the IL-Ilp polypeptide or for producing gene knock out animals to study the IL-Ilp polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and disease processes (conversely, gene therapy protecols may be used to supplement a patients production of the polypeptide or to rectify mutations that lead to the production of in active peptides). The peptides produced may be used to screen for and produce modulators (e.g. antibodies) of IL-Ilp protein expression and activity which may be use to treat disenders associated with inappropriate IL-Ilp expression and activity, such as inflammatory disorders, asthma, arthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSFVGENSGVKMGSEDWEKDEPOCCLEDPAGSPLEPGPSLPTMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLBSAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, interleukin-1 homologue, IL-1H4, inflammation, septicaemia, autolmmune disease, inflammatory bowel disease, psoriasis, arthritis, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease, allergy, asthma, restenosis, brain injury, AIDS, bone disease, osteoporosis, cancer, congestive heart failure, atherosclerosis, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSFVGENSGVKMGSEDWEKDEPOCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                             Nucleic acids encoding interleukin-1-like polypeptides, useful for preventing and treating e.g. inflammation, asthma and psoriasis.
                                                                                                                                                                                                      An isolated nucleic acid molecule encoding an interleukin-1-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1130; DB 3; Length 218; Pred. No. 6e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human interleukin-1 homologue IL-1H4.
                                                                                                                                                                           Claim 22; Fig 19; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB28266 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.8%;
98.2%;
99US-0129122P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 214; Conservative
                            (GETH ) GENENTECH INC
                                                                                      WPI; 2000-452395/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                         Pan J;
                                                                                                     N-PSDB; AAA51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 218 AA;
 13-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2001
                                                        Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB28266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB28266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-1 homolog useful for treating conditions such as chronic and acute inflammation, septicemia, autoimmune diseases ischemia, acute respiratory disease, allergies, and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 useful for treating conditions such as chronic and acute inflammation, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis, and arthritis). transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease, allergies, asthma, restenosis, brain injury, AIDS, bone disease, osteoporosis), cancer, congestive heart failure, atherosclerosis, and Alzheimer's disease, related to either an excess of, or an underexpression of, IL-1H4 polypeptide activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPF1FYRAQVGSRNMLESAAHPGWF1CTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic; immunosuppressive; antipsoriatic; antiarthritic; cytostatic; antiHIV; cerebroprotective; antiasthmatic; vasotropic; vulnerary; osteopathic; immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1130; DB 3; Length 218;
Pred. No. 6e-118;
1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-1 homologue (IL-1H4) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 28-29; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB85136 standard; protein; 218
                                                                                                                                       SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.8%;
98.2%;
14-APR-2000; 2000WO-US010207
                                                                     99US-00293625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; vaccine.
                                                                                                                                                                                                             Mcdonnel1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                   WPI: 2000-687155/67
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAC66727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 218 AA;
```

ô

120

```
gene therapy; psoriasis; diagnosis.
Antipsoriatic protein sequence #686.
                                                                                                                                                                                                                                                                                                           N-PSDB; ADN05011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 218 AA;
                                                                                         WO2004028479-A2
                               antipsoriatic;
                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2000
                                                                                                                     08-APR-2004
                                                                                                                                                                                                                                              Bodary S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY71084
   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides an isolated interleukin-1 homologue, IL-1H4 polypeptide can be expressed by standard complypeptide. The IL-1H4 polypeptide, polymocleotides and modulators are useful for treating chronic and acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory bowel disease, psoriasis and arthritis), transplant rejection, graft versus host disease, infection, stroke, ischemia, acute respiratory disease synforme, allergies, asthma, restenois, brain injury, AIDS, bone diseases (e.g., osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive heart failure, antherosclerosis and Alzheimer's disease. The IL-1H4 polymucleotides are useful as diagnostic reagents and for chromosome identification. The present sequence represents the IL-1H4 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                          'note= "specifically claimed mature protein (AAB85138)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDKDKGQSHPSLQLKKEKIMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                       Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute inflammation, septicemia, autoimmune diseases, transplant rejection, graft versus host disease, stroke, ischemia, allergy and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1130; DB 4; Length 218;
Pred. No. 6e-118;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                 1. .20
/note= "signal peptide"
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                 Young PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN05012 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 29; 30pp; English.
                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.8%;
                                                                                                                                                                                                                   99US-00452140
                                                                                                                                                                                       30-NOV-2000; 2000WO-US032521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 98.2
Matches 214; Conservative
                                                                                                                                                                                                                                                                                 Mcdonnell PC,
                                                                                                                                                                                                                                                                                                              WPI; 2001-389949/41.
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF84120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 218 AA;
                                                                                                                            WO200140247-A1
                                                                  Cleavage-site
                                                                                                                                                                                                                     01-DEC-1999;
                                                                                                                                                        07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                 Kumar S,
                                 Peptide
                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
ADN05012
```

```
Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis; psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer; anaemia; inflammatory bowel disease; acute neuropathology; shock; chronic neuropathology; respiratory disease syndrome; restenosis; acquired immune deficiency syndrome; AlDS; antiinflammatory; cytostatic; anti-arthritic; anti-psoriatic; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel polynuclectide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                      Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIHDODHKVIVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                              New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                   Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.8%; Score 1130; DB 8; 98.2%; Pred. No. 6e-118; ive 1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                             claim 9; SEQ ID NO 1406; 3069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human zilla4-E200D variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71084 standard; protein; 218 AA
                                                                                                                                        Jackman J,
                                              25-SEP-2002; 2002US-0414006P.
25-SEP-2003; 2003WO-US030907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 214; Conservative
                                                                                            (GETH ) GENENTECH INC
                                                                                                                                           Clark H,
                                                                                                                                                                                                               WPI; 2004-305105/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
```

ö

120

180

01-JUL-2004 (first entry)

ద

ઠે

원 ઠે 셤 ò 셤

ò

120

```
cytostatic; antianaemic.
                        Homo sapiens.
                                                                                                                  27-OCT-1998;
27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2000
                                                                    07-AUG-2003
                                                                                                                                                                                                                                                            anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY70933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                         West RR,
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                        The present sequence is a variant of human interleukin (IL)-1 homolog zilla4 protein, consisting of Asp in place of Glu at position 200. The replacement of Glu (200) with Asp results in attenuation of pro-inflammatory activity of zilla4 protein. The zilla4 proteins modulate inflammation and other immunological processes and are therefore useful for treatment of arthritis, psoriasis, septic shock, graft-versus-host disease and leukaemia. Other diseases that may be modulated by zilla4 proteins include cancer, anaemia, inflammatory bowel disease, acute and chronic neuropathologies, shock, respiratory disease syndrome, restenosis and acquired immune deficiency syndrome. Note: The present sequence is not shown in the specification but is derived from human zilla4 protein sequence shown in figure-2 (AAY70927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, interleukin-1 homologue, IL-1; zilla4; immune response;
inflammatory disease; cancer; anaemia; immunomodulator; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                   treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
disease, leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                        [mmunomodulatory interleukin-1 homolog zilla4 proteins, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.6%; Score 1127; DB 3; Length 218; 97.7%; Pred. No. 1.3e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNCNEPVGVTDKFENRKHIDFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
anti-anaemic, neuroprotective; vasotropic, variant, anti-human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH89067 standard; protein; 218
                                                                                                                                                                           Z;
                                                                                                                                                                                                                                                                     Claim 3; Page; 88pp; English.
                                                                                                      99WO-US025038
                                                                                                                              98US-00179614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 97.7 Matches 213; Conservative
                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zilla4 polypeptide.
                                                                                                                                                                          Sheppard PO,
                                                                                                                                                                                                 WPI; 2000-350740/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 218 AA;
                                                         WO200024899-A2
                                    Homo sapiens
                                                                                                      27-OCT-1999;
                                                                                                                              27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-2004
                                                                                04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH89067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  임
```

```
New interleukin-1 homolog Zilla4 protein, useful for modulating an immune response and for treating diseases, e.g., inflammatory diseases, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of human interleukin-1 (IL-1) homologues designated zilla4, and the polynucleotide sequences that encode them. The gene encoding human zilla4 is located on chromosome 2. Also disclosed is a method of making these proteins and a method of modulating an immune response. The proteins are useful for treating diseases such as inflammatory diseases, cancer, and anaemia. The present sequence represents human zilla4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLQSAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLBSAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis; psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer; anaemia; inflammatory bowel disease; acute neuropathology; shock; chronic neuropathology; respiratory disease syndrome; restenosis; acquired immune deficiency syndrome; ALDS; antiinflammatory; cytostatic; anti-arthritic; anti-psoriatic; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1127; DB 7;
Pred. No. 1.3e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID NO 2; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zilla4-E200K variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70933 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                          Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.6%;
                                                                                                                          22-NOV-2002; 2002US-00302554
                                                                                                                                                                                          98US-0105824P
99US-00428118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213; Conservative
                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                          Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-897576/82.
N-PSDB; ADH89066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 218 AA;
US2003148467-A1
```

ö

120

34-MAY-2000

RR,

West

```
The present invention relates to the isolation of human interleukin-1 (II homologues designated zilla4, and the polynucleotide sequences that encode them. The gene encoding human zilla4 is located on chromosome 2. Also disclosed is a method of making these proteins and a method of modulating an immune response. The proteins are useful for treating diseases such as inflammatory diseases, cancer, and anaemia. The present sequence represents a variant human zilla4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                            New interleukin-1 homolog Zilla4 protein, useful for modulating an immur
response and for treating diseases, e.g., inflammatory diseases, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCDKDKGOSHPSLOLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1126; DB 7;
Pred. No. 1.7e-117;
2; Mismatches 3;
                                                                                    /note= "Encoded by AAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 14; 44pp; English
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY95299 standard; protein; 218
                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.5%;
                                                                                                                                                                                                                                 98US-0105824P.
99US-00428118.
                                                                                                                                                                                               22-NOV-2002; 2002US-00302554
                                                                                                                                                                                                                                                                                                                         Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                         West RR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-897576/82
                                                                   Misc-difference 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADH89074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 218 AA;
                                                                                                                        US2003148467-A1
sapiens.
                                                                                                                                                                                                                                 27-OCT-1998;
27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2000
                                                                                                                                                            07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         anemia.
                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY95299
                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; interleukin-1 homologue; IL-1; zilla4; immune response;
inflammatory disease; cancer; anaemia; immunomodulator; antiinflammatory;
cytostatic; antianaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a variant of human interleukin (IL)-1 homolog zilla4 protein designated zilla4-B200K. The replacement of Glu (200) with Usy regults in change in activity from agonist to antagonist. The zilla4 proteins modulate inflammation and other immunological processes at therefore useful for creatment of arthritis, psoriasis, septic shock, graft-versus-host disease and leukaemia. Other diseases that may be modulated by zilla4 proteins include cancer, anaemia, inflammatory bowel disease, acute and chronic neuropathologies, shock, respiratory disease syndrome, restenosis and acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                              Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
disease, leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNCNEPVGVTDKFENRKHIEFSPQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1126; DB 3;
Pred. No. 1.7e-117;
2; Mismatches 3;
   anti-anaemic; neuroprotective; vasotropic; anti-human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 77-78; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH89075 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human zilla4 variant protein #5.
                                                                                                                                                                                                                                                                         Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.5%;
                                                                                                                                                             99WO-US025038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 213; Conservative
                                                                                                                                                                                                                                                                         Sheppard PO,
                                                                                                                                                                                                                                                                                                          2000-350740/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD00212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 218 AA;
                                                                                          WO200024899-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-2004
                                                          Ношо варіепв
                                                                                                                                                                 27-OCT-1999;
                                                                                                                                                                                                   27-OCT-1998;
```

ö

Gaps

ö

Length 218; Indels 9 9

an immune

180

120 120

```
Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1; testis-derived zeta variant; therapy; inflammation; fever.
                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-1 zeta splice variant TDZ.1,
```

ADH89075;

61

셤 ሯ

ઢ

g

Query Match Local 181

g ò 셤

ò

181

RESULT 13

ADH8907

```
AAY91885 standard; protein; 218 AA.
                                                                      (first entry)
                                                                      19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Timans JC;
                                    AAY91885;
                                                                                                                                                                                                              Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
 The present sequence is that of splice variant TDZ.1 (testis-derived zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is expressed most strongly in the kidney, skeletal muscle, testis, prostate, covary, colon, small intestine, liver, placenta, lung, tonsil, foetal liver, lymph node and bone marrow. The invention is directed to novel, culfied and isolated IL-1 zeta, its splice variants and Xrec2 purified and isolated IL-1 zeta, its splice variants and Xrec2 colypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22) colypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22) colypeptides, and their uses. The polypeptides can be used to study cellular processes such as immune regulation, cell proliferation, cell migration, cell-to-cell interaction and inflammatory responses, to identify proteins associated with IL-1 zeta, to screen for potential inhibitors, and to prepare antibodies. In particular, they can be used to activate and/or inhibit the activation of vascular endothelial cells to produce IL-6, induce and/or inhibit the induction of local induction of prostaglandins, nitric oxide synthetase, and vor inhibit the upregulation of metalloproteases, and upregulate and/or inhibit the upregulation of metalloproteases, and upregulat endothelial cells cometalloproteases, and upregulat endothelial cells cometalloproteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                   TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for identifying genes associated with diseases such as glaucoma, and insulindependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                      solated interleukin-1 (IL-1) zeta nucleic acids and splice variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 1121; DB 3; Length 218; 97.7%; Pred. No. 6.1e-117; ive 1; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 11; 87pp; English.
                                                                                                         99WO-US029549.
                                                                                                                                          98US-0112163P.
99US-0164675P.
                                                                                                                                                                                                                                   Born TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                              (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                    WPI; 2000-442387/38.
                                                                                                                                                                                                                                 Smith DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                     N-PSDB; AAA27920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 218 AA;
                                   WO200036108-A2.
   Homo sapiens
                                                                                                                                          14-DEC-1998;
10-NOV-1999;
                                                                                                         14-DEC-1999;
                                                                      22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                 Sime JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

```
The present sequence is an alternative primate interleukin-1 like molecule, designated IL-1zeta. The 12 beta strands, indicated in the features table, fold into a beta-trefoil fold. The specification claims an isolated or recombinant polypeptide that: (a) specifically binds polyclonal antibodies generated against at least a 12 consecutive amino acid segment of IL-1zeta (see AAY91884) or its allelic variant (see AAY91885); and (b) comprises at least one sequence selected from: AAY91885) and (b) comprises at least one sequence selected from segment is chosen from AAY91907-18 or AAY91919-21. IL-1zeta is likely t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "forms a loop which is part of a primary binding segment to the IL-1 receptor type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful for diagnostic and therapeutic purposes, comprises a 128 amino acid
                                          Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever; hypoglycemia; plasma iron; plasma zinc; acute liver response; plasma copper.
Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= beta_strand_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= beta_strand_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 103-104; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      91. .96
/label= beta_strand_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta_strand_9
                                                                                                                                                                                                                                                                                                                          /label= beta_strand_2
                                                                                                                                                                                                                                                                                                                                                         76. .80
/label= beta_strand_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta_strand_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131. .136
/label= beta_strand_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta_strand_8
                                                                                                                                                                                                                                                                       /label= beta_strand_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta_strand_5
                                                                                                                                                                                                                     cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US020868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .161
/label= br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163. .169
/label= be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-283588/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA08513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200017363-A2
```

ઠે 임 ઠે 셤 ò 셤 8 t

```
play a role in systemic inflammatory reactions, such as fever, hypoglycemia, reduced plasma iron and zinc, the acute response of the liver, and increase plasma copper. IL-1-zeta binding compounds (comprising antigen binding sites) and IL-1-zeta polypeptides are also useful for both diagnostic and therapeutic purposes
              ន្តន្តន្តន្តន្ត
```

Sequence 218 AA;

Gaps ö Query Match
96.6%; Score 1116; DB 3; Length 218;
Best Local Similarity 97.2%; Pred. No. 2.2e-116;
Matches 212; Conservative 1; Mismatches 5; Indels

1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF

ò 셤 셤

ઠે

셤

ઠ

9

120 

ઠે 셤

Search completed: September 29, 2005, 11:12:56 Job time: 68.5 secs

THIS PASE OF THE USERION

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

- protein search, using sw model OM protein September 29, 2005, 11:04:58; Search time 25.5 Seconds (without alignments) 822.559 Million cell updates/sec Run on:

US-10-695-195-2 1155 1 MSFVGENSGVKMGSEDWEKD.....IEFSPQPVCKAEMSPSEVSD 218 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	interleukin-1 rece	interleukin-1 beta	interleukin-1 beta	interleukin-1 beta	interleukin-1 beta				interleukin-1 beta	hypothetical prote	-	hypothetical prote	hypothetical prote	ø	interleukin-1 alph	L-fuculose-phospha	probable membrane	hypothetical prote		hypothetical prote		hypothetical prote	0	hypothetical prote					
	ID	JC7104	A44610	A30368	A39386	A54377	C40956	538373	823010	JN0724	ICB01B	155969	ICHU1B	JC5646	A30584	T24522	E71806	T17291	C87358	D96504	ICMS1	B72299	867053	T19372	145857	T24158	T24157	D86164	C86278	D86254
	108	. ~	~	~	~	~	N	ď	-	-	Н	~	Н	~	~1	~	8	7	~	~	-	-	~	~	N	7	7	7	7	7
		155	178	177	180	177	178	267	266	267	266	269	269	214	268	425	1001	845	859	772	270	236	776	351	215	2584	2606	571	673	851
مد	Match	14.2	13.9	13.5	13.5	13.1	12.8	10.5	10.3	10.0	9.0	8.7	8.2	7.4	7.4	7.4	7.4	7.3	7.3	7.2	7.0	6.9	6.9	6.9	6.8	6.8	6.8	9.8	6.8	6.8
	Sc	163.5	160	155.5	55	151.5	147.5	121	118.5	115	103.5	100.5	94.5	98	98	85	85	84.5	8	83	81	80	80	79	78.5	78.5	78.5	78	78	78
		-	7	ю	4	ഹ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote	hypothetical prote	acetyl-CoA carboxy	T-cadherin precurs	T-cadherin 2 - chi	transcription-repa	hypothetical prote	oligoendopeptidase	oligopeptidase (im	KTR3 protein - yea	ABC transporter-li	AMP deaminase (EC	mucin, tracheobron	hypothetical prote		hypothetical prote
T45635	T34342	S46200	IJMSCT	151206	E64712	T04426	E72114	H86507	S34031	T46101	I39444	A48292	T48794	T02846	B96592
~	~	7	Н	~	~	7	7	7	~	~	7	~	~	~	0
547	862	1561	712	717	666	1405	611	611	404	737	747	1118	211	627	914
6.7	6.7	6.7	6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5
77.5	77.5	77.5	77	77	77	77	76.5	76.5	16	16	16	16	75.5	75.5	75.5
0	Ę	32	33	34	22	36	37	8	39	0	급	2	2	4	5

## ALIGNMENTS

RESULT 1

interleukin-1 receptor antagonist - human ('Species Homo appiens (man) ('Species Homo appiens ('Species Homo antagonist ('Species Home antagonist ('Species Homo antagonist ('Species Hom

A;Map position: 2q14 C;Keywords: macrophage

9 Gaps 37; DB 2; Length 155; 48; Indels Query Match
14.2%; Score 163.5; DB 2
Best Local Similarity 32.9%; Pred. No. 8.2e-08;
Matches 50; Conservative 17; Mismatches 48

106 22 9 FRMKDSALKVLYLHNNQL------LAGGLHAGKVIKGEEISVVPNRWLDA 60 FSIHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKG-ઠે g 107 --SLILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS 163 ò

53 SLSPVILGVQGGSQCLSC--GVGQ-EPTLTLEPVNIMELXLGAKES--KSFTFYRRDMGL 107 : ||||:||||:|| : || || : || 139 108 TSSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139 164 RNMLESAAHPGWFICTSCNCNEPVGVTDKFEN 195 셤 ઠે

A44610

셤

interleukin-1 receptor antagonist precursor - mouse
NyAlternate names: IL-IRa
() Species: Was musculus (house mouse)
() Species: Was musculus (house mouse)
() Date: 09-58p-1994 #sequence revision 09-58p-1994 #text\_change 09-Jul-2004
() Accession: A44610; B40956; A49031; IS6106; IS5270
() Accession: A44610; B40956; A49031; IS6106; IS5270
() R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
() A, Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophical control and expression of musine interleukin-1 receptor antagonist in macrophical control and A44610
() A, Reference number: A44610; MUID:91316273; PMID:1830498
() A, Residence : UNIPROT:P25085; GB:M64404; NID:9198296; PIDN:AAA39277.1; PID:91982-R; Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson

```
A; Gene: GDB: IL1RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Molecule type: mRNA
A;Residues: 1-178 <RES.
A;Residues: 1-178 <RES.
A;Cross-references: GE:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A;Reference number: 152970; MUID:94271931; PMID:8003626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-1 receptor antagonist secreted form precursor - human (5.Species: Homo sapiens (man) (5.Species: Homo sapiens (man) (5.Date: 07-Jun-1990 #text change 09-Jul-2004 (5.Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text change 09-Jul-2004 (5.Accession: A40956; 137894; Ā30368; 808160; 808159; A37822 (5.Accession: A40956; I137894; Ā30368; 1091 (Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991 (A.Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: A,Reference number: A40956; MUID:91271363; PMID:1828896 (A.Mocession: A40956 (A.Mocession: A40956) (A.Mocession: A10956) (A.Mocession: A10956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues 12-178 <RHU>
A; Cross-references: GB:864082; NID:9238584; PIDN:AAB20265.1; PID:9238585
A; Residues: 23-178 <RHU>
A; Bxperimental source: periconeal macrophages, ICR strain
A; Bytates sequence extracted from NCBI backbone (NCBIN:64082) NCBIP:64085)
B; Rabadi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J Immunol. 146, 4228-4233, 1991
A; Ritche Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mappin
A; Reference number: I56106; MUD:91250712; PMID:1828262
                                                A,Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family.
A,Reference number: A40956; MUID:91271363; PMID:1828896
                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A;Title: Cloning, heterologous expression and characterization of murine interleukin 1
A;Reference number: A49031; MUID:92037824; PMID:1834470
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 FSIHDQDHKVLVLDSGNLIAVPDKNYIR-PRIFFALASSLSSASAEKGSLILLGVSKGEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFIC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Gene: IL-1rn
A;Introns: 40/2; 70/1; 107/3
C;Superfamily: interleukin-1
C;Keywords: cytckine receptor
F;1-26/Domain: aignal sequence #status predicted <SIG>
F;27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RE2>
A;Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Score 160; DB 2; Length 178; 32.7%; Pred. No. 2.1e-07; Artive 23; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
5232-5236, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 TSCNCNEPVGVTDKFENRKHI-EFSFQ 204
     Sci. U.S.A. 88,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                     A, Accession: B40956
A, Molecule type: DNA
A, Residues: 7-178 <EIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
A,Cross-references: UNIPROT:P18510; GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386 R;Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, J. Sycokine 4, 83-89, 1992 B. A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist A,Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist A,Reference number: 137894; MUID:92338323; PMID:1385987
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Modecule type: DNA
A; Residues: 1-177 < LEN>
A; Cross-references: RNBL: X64532; NID: 933798; PIDN: CAA45832.1; PID: 933799
B; Cross-references: RNBL: X64532; Num, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; T. Mature 344, 633-638, 1990
A; Title: Purification, cloning, expression and biological characterization of an interly A; Reference number: A30368; MUID: 90220867; PMID: 2139180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-177 < CAR:
A; Residues: 1-177 < CAR:
A; Cross - references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
A; Note: parts of this sequence, including the amino end of the mature protein, were con:
R; Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
Nature 343, 341-346, 1990
A; Tritle: Primary structure and functional expression from complementary DNA of a human
A; Reference number: S08160; MUID:90136921; PMID:2137201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-17, <EIE.>
A;Residues: 1-17, <EIE.>
A;Considues: 1-17, <EIE.
A;Considues: 1-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R;Bienkowski, M.J.; Bessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde
B;Bienkowski, M.J.; Bessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde
A; Biol. Chem. 265, 14505-14511, 1990
A;Title: Purification and characterization of interleukin 1 receptor level antagonist p
A;Reference number: A37822; MUID:90354444; PMID:2143761
A;Accession: A37822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extracellular protein; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Kerwords: alternative splicing; cytokine receptor; extracellular protein; gl:
F;1.25/Domain: signal sequence #status predicted <SIGs
F;26.177/Product: interleukin-1 receptor antagonist #status experimental <WAT>
F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 KSLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSSASAEKGSLILL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 GVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: culture medium, PMA-stimulated THP-1 cells C, Comment: For an alternative splice form, see PIR:A39386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 155.5; DB 2
Pred. No. 5.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 26-52;70-77;122-127;170-175 <BIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
A;Introns: 39/2; 69/1; 106/3
C;Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 HPGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                            A;Accession: I37894
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.5%;
30.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A30368
```

7;

Gaps

15;

DB 2; Length 177; 55; Indela

```
C;Accession: C40956
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson R;Eisenberg, Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family A;Reference number: A40956; MUID:91271363; PMID:1828896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA.
A;Residues: 1.178 <ELS.
A;Cross-references: UNIPROT:P25086; GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g20492
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterTeukin-1 beta precursor - pig
Cispecies: Sus scrofa domestica (domestic pig)
Cjate: 20-May-1994 #sequence_revision 01-bec-1995 #text_change 09-Jul-2004
Cjate: 20-May-1994 #sequence_revision 01-bec-1995 #text_change 09-Jul-2004
Cjacession: 838373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Op:
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Op:
R;Vandenbroeck, CDMA construction, expression in Escherichia coli and genetical
A;Reference number: 838373 MUD:94039070; PMID:8223584
A;Accession: 838373
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 VSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 FSIHDQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSSASAEKGSLILLGVSKGEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLYCDK--DKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | : | : | : | : | : | : | : | | ERIMDVNQKTFYLRNNQLVA----GYLQGPNA--KLEERIDVVPLEP-QLLFLGIQRGKL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-1 receptor antagonist precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASABKGSL-----ILLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 FRIWDTNQKTFYLRNNQLIA----GYLQ------GPNTKLEEKIDMVPIDFRNVFLG
A;Residues: 1-177 <COT>
A;Residues: 1-177 <COT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #eratus predicted <SIG>
F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%; Score 147.5; DB 2; 29.5%; Pred. No. 3e-06; tive 22; Mismatches 53;
                                                                                                                                                                                                                                                                                                                            13.1%; Score 151.5; DB 2
31.9%; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 31.9%; Pred. No. 1.3e tes 43; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||:||: : || :|:
143 PGWFLCTTLEADHPVSLTN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 PGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||: ::|| :|:
146 LCTALEADQPVSLTN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: C40956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/MOJECULE TYPE: MRNA
A/Residues: 1-3,25-180 <HAS>
C; Comment: For an alternative splice form, see PIR:A30368
C; Cometics: Transitive splicing of the properties of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: colon tissue
A; Experimental source: colon tissue
A; Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
B; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Maeda
Immunology 77, 235-224, 1992
A; Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. Prod
A; Reference number: 146729; MUID:93052512; PMID:1427977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-180 <RES.
A; Residues: 1-180 <RES.
A; Cross-references: UNIPROT: P18510; EMBL: X84348; NID: 91008970; PIDN: CAA59087.1; PID: 9100
R; Habkill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.;
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A; Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
A; Reference number: A39386; MUID: 91219436; PMID: 1827201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-1 receptor antagonist secreted form precursor - rabbit c; Species: Oryctolagus cuniculus (domestic rabbit) c; Species: Oryctolagus cuniculus (domestic rabbit) c; Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: A54377; 146729 K; Cominolli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T. J. Biol. Chem. 269, 6562-6971, 1994 A; Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara A; Reference number: A54377; MUID: 94165101; PMID: 7509813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-17, <COM>
A; Cross-references: UNIPROT: P26890; GB:S68977; NID:G545740; PIDN:AAB30093.1; PID:g545741
A; Experimental source: colon tissue
                                                                                                                                                                                                                                                 Cjaccession: 137893; A39386

Cjaccession: 137893; A39386

W.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan J. Exp. Med. 182, 623-628, 1995

A; Title: Cloning and characterization of a new isoform of the interleukin 1 receptor and A; Reference number: 137893; MUID:9535865; PMID:7629520

A; Recession: 137893

A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 GVSKGEFCLYCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-1 receptor antagonist, long intracellular splice form - human N;Contains: interleukin-1 receptor antagonist, short intracellular splice form C;Species: Homo sapiens (man) C;Species: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 KSLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIR-PBIFFALASSLSSASAEKGSLILL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.5%; Score 155.5; DB 2; Best Local Similarity 30.7%; Pred. No. 5.4e-07; Matches 43; Conservative 26; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 HPGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Accession: I46729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

ŝ 112

Gaps

23;

53; Indels

Length 178;

```
F;114-266/Product: interleukin-1 beta #status predicted <MAT>
                                                  Query Match
Best Local Similarity 28.8%
Marches 38, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 YISTSQIEEKPV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 FICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JL0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: JN0724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternate names: hematopoietin-1; IL-1 beta
() Alternate names: hematopoietin-1; IL-1 beta
() Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
() Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
() Space: Ob-Jun-1994 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
() Accession: S2010; S43047; S13092; B61246
() A. Secow, H. F.; Rothel, J. S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
() A. Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
() A. Reference number: S23010; MUDD:92119335; PMID:1840515
() A. Rocession: S23010
() A. Rocession: S3047
() A. Residues: 1-266 < SSD.
() A. Rocession: S43047
() A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-144,'L',146-266 <AND>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
                                          A;Cross-references: UNIPROT:Q29082; EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g4079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Molecular cloning and characterization of ovine IL-lalpha and IL-lbeta
A,Reference number: A61246; MUID:92120716; PMID:1769692
                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                        HKVLVLDSGNLIAVPD--KNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCLYC-D 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDKGOSHPSLOLKKEKLMKLAAOKESARRPFIFYRAOVGSRNMLESAAHPGWFICTSCNC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 KDEPQ-----CCLEDPA---GSPLEPGPSL---PTMNFVHTSRKVKSLNPKKFSIHDQD
                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-61,'S',63,'A',65-144,'L',146-266
A;Cross-references: EMBL:X54796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for residue 62 as Arg
                                                                                                                                                                                                                    Query Match 10.5%; Score 121; DB 2; Length 267; Best Local Similarity 27.2%; Pred. No. 0.0014; Matches 50; Conservative 32; Mismatches 78; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: the authors translated the codon AGT for residue R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D. Immunology 74, 453-460, 1991
                                                                 C;Genetics:
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C;Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-1 beta precursor - sheep
A;Residues: 1-267 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 NEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: B61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                            임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
C,Accession: JN0724
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
A;Hitle: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be A;Reference number: JN0724; MUID:93314975; PMID:8325511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
A; Residues: 1-267 - KHUE.
A; Cross-references: UNIPROT: P26889; GB: M86725; NID: g164607; PIDN: AAA02584.1; PID: g164608
A; Experimental source: alveelar macrophage
C; Comment: This protein is a pleiotropic cytokine that mediates a variety of processes 1
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-1a
C; Superfamily: interleukin-1
C; Superfamily: interleukin-1
C; Superfamily: interleukin-1
C; Superfamily: interleukin-1
C; Meywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F; 115-267/Product: interleukin-1 beta #status predicted <111.>
F; 77/Binding site: myristate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NyAlternate names: hematopoietin-1; IL-1 beta
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 3.1-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: JL0010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S., M.J. Innuol. 125, 429-437, 1988
A;Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
A;Reference number: A94695; MUID:88318652; PMID:3261832
                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                           59 KFSIHDQDHKVLVLDGG---NLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 VKSLNPKKFSIHDQDHKVLVLDSGNLIAVPD--KNYIRPEIFFALASSLSSASAEKGSLI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 LLGVSKGEFCLYC-DKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 KCKLODREQKSLVLDSPCVLKALHLPSQEMSR-EVVFCM-SFVQGEERDNKIPVALGIRD 177
                                                                                                                                                                                                                                                                                                                                                          116 GEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                          9
;; Score 118.5; DB 1; Length 266;
;; Pred. No. 0.0023;
26; Mismatches 59; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 10.0%; Score 115; DB 1; Length 267; Similarity 28.1%; Pred. No. 0.0049; 39; Conservative 27; Mismatches 61; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 SAAHPGWFICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALYPNWYISTSQAEQKPV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-1 beta precursor - bovine
             10.3%;
28.8%;
```

DB 1; Length 269;

```
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <1L1>
                                                                                                                                                                                                                                          Query Match

8.7%; Score 100.5; DB 1;
Best Local Similarity 23.2%; Pred. No. 0.11;
Matches 48; Conservative 38; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: I51852
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-269 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A93361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecul type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule: 118-269 < LDAU> C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive. C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lackin-lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P10749; GB:M15131; NID:9198293; PIDN:AAA39276.1; PID:9309398 R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M. Nucleic Acids Res. 14, 9955-9963, 1986 Nucleic Acids Res. 17 me murine interleukin 1-beta gene: structure and evolution. A;Reference number: A24719; MUID:87117546; PMID:3492706
                               A;Molecule type: mRNA
A;Residues: 1-266 <MAL>
A;Residues: 1-266 <MAL>
A;Cross-retences: UNIPROT: P09428; GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
A;Cross-retences: UNIPROT: P09428; GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
Nucleic Acids Res. 16, 9054, 1988
A;Title: The nucleotide sequence for the CDNA of bovine interleukin-1 beta.
A;Reference number: S01380; MUID:89016591; PMID:3262866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-269 <TEL>
A; Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667
R; Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I.
FEBS. Lett. -778, 98-102, 1991
A; Title: Reduction of biological activity of murine recombinant interleukin-lbeta by sel
A; Reference number: S13029; MUID:91130610; PMID:1993481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: Molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Ke_words: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen P;114-266/Product: interleukin-1 beta #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 KFSIHDODHKVLVLDSGNLIAVPD--KNYIRPEIFFALASSLSSASAEKGSLILLGVSKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KCKLQDREQKSLVLASPCVLKALHLLSQEMNREVVFCM-SFVQGEERDNKIPVALGIKDK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 BPCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.0%; Score 103.5; DB 1; Length 266; Best Local Similarity 26.7%; Pred. No. 0.057; Matches 35; Conservative 25; Mismatches 64; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 ISTSQIEERPV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 ICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S13029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: IL-1-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
interlaukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence revision 15-May-1998 #text_change 09-Jul-2004
C;Accession: A25542; A29019; Ā94023; A93361; I51852; I65200; I38132; B27616; A01848; S1
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a re
A;Reference number: A25542; MUID:87040762; PMID:3490654
A;Accession: A25542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A.2-3-4.

A; Molecule type: DNA; mRNA
A; Residues: 1-5, K', 7-269 cCLA>
A; Cross-references: UNIPROT: P01564; GB: X04500; NID: g33788
A; Cross-references: UNIPROT: P01564; GB: X04500; NID: g33788
A; Cross-references: UNIPROT: P01564; GB: X04500; NID: g33788
A; Cross-reference had codon AdG for 6-Lys, the DNA sequence had GAG for 6-Glu R; Bensi, G; Raugei, G; Palla, E; Carinci, V; Buonamassa, D.T.; Melli, M.
A; Reference number: A29019; MUD: 87248099; PMID: 2954882
A; Reference number: A29019; MUD: 87248099; PMID: 2954882
A; Molecule type: DNA
A; Residues: 1-269 cabs
A; Molecule type: DNA
A; Residues: 1-269 cabs
A; Cross-references: GB: MID: 9107-7911, 1984
A; Residues: 1-269 cabs
A; Reference number: A94023; MUD: 85088517; PMID: 6083565
A; Reference number: A94023; MUD: 85088517; PMID: 6083565
A; Residues: 1-5, K', 7-269 cabs
A; Residues: 1-5, K', 7-269 cabs
A; Cross-references: GB: K02770; NID: g186268; PIDN: AAA36106.1; PID: g307043
A; Ross-references: GB: K02770; NID: g186268; PIDN: AAA36106.1; PID: g307043
A; Cross-references: GB: K02770; NID: g186268; PIDN: AAA36106.1; PID: g307043
A; Reference number: A93361; MUD: 85240547; PMID: 2989698
A; Title: Cloning, sequence and expression of two distinct human interleukin-1 complemes
A; Reference number: A93361; MUD: 85240547; PMID: 2989698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were confix R;Webb A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; F. Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor CDNA.
A;Reference number: I51852
                                                                                                                                                                      94 SFIFEEEPILCDS--WDDDD----YR 126
                                                                                                                                                                                                                                                                IHDODHKVLVL-DSGNLIAVP-DKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFC 119
                                                                                                                                                                                                                                                                                                                                                          127 LRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSNDK-IPVALGLKGKNLY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKFS
Gaps
35;
Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 SQAEHKPVFLGNN-SGQDIIDFTMESV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCNCNEPVGVTDKFENRKHIEFSFQPV 206
```

φ

9

```
equine interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-1 beta precursor - rabbit
N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fa
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-May-1389 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: A27714; A30584; Ju0082; A32166
C;Accession: A27714; A30584; Ju0082; A32166
B;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiat
A;Reference number: A27714; MUID:88134238; PMID:2449207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q28386; DDBJ:D42165; NID:92463549; PIDN:BAA22528.1; PID:924 C;Comment: This protein mediates a variety of physiological response to infections and synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce C;Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Species: Bquus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: JC5646
R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa, A;Kato, H.; Ill-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-1
A;Reference number: JC5646; MUID:97080493; PMID:8921838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 SAEKGSLILLGVSKGEFCLYC--DKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 SAEKGSLIILGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQV 161
                             experimental
                                                                                                                                                                                                                                                                                                                                                                   43 MNFVHTSRKVKSLN-PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSA
                                                                                                                                                                                                                                                                                                       FVHTSRKVKSLNPKKFSIHDQDHKVLVLDSG--NLIAVPDKNY-IRPEIFFALASSLSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 MSIIVAVEKLKKIPVPCSQAFQDDDLRSLF-----SVIFEEVVFCMSFVQGEE
                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                           Length 269;
                     F;76/Binding site: myristate (Lys) (covalent) (partial) #status (F;123/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 86; DB 2; Length 214; 23.3%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Indels
                                                                                                                                       5; DB 1;
0.39;
                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A27714
A;Status: not compared with conceptual translation
                                                                                                                                           8.2%; Score 94.5; D
28.4%; Pred. No. 0.39
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 EINNKLEFESAQFPNWYISTSQAENMPV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 QVGSRNMLESAAHPGWFICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 GSRNMLESAAHPGWFICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGNVEFESAMYPNWYISTSQAEKSPV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.34
Matches 34; Conservative
                                                                                                                                                                                                                           42; Conservative
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: JC5646
A, Molecule type: mRNA
A, Residues: 1-214 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-268 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
JC5646
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
A; Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
B; Cross-references: EMBL:X56087; NID:g3562; PIDN:CAA39567.1; PID:g35663
B; Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic
A; Reference number: A90732; MUID:88184226; PMID:3281727
A; Recession: B27616
A; Molecule type: protein
A; Residues: 117-123, X*, 125-126, X*, 128 < ZSE5
A; Revenson, FT; Bursten, S.L.; Fanton, C; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A; Title: The 31-kDa precursor of interleukin lalpha is myristoylated on specific lysines
A; Reference number: A48293; MUID:9314250; PMID:8346241
A; Contents: annotation; myristylation of lysines
A; Rinduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
B; Contents: annotation; myristylation of lysines
A; Reference number: S19608; MUID:92110334; PMID:837336
A; Contents: annotation: type 1 IL-1 receptor interaction site
A; Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
A; Richer modification of Arg-120 by phenylglyoxal blocks receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Contents: annotation
B;Finzel, B.C.; Matenpaugh, K.D.; Einspahr, H.M.
Bipfinzel, B.C.; Matenpaugh, K.D.; Einspahr, H.M.
Bipfinzel, B.C.; Matenpaugh, K.D.; Einspahr, H.M.
A;Reference number: ASO104; PDB:111B
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
A;Refinzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspahr, J. Mol. Biol. 209, 779-791, 1989
A;Filzel, Crystal structure of recombinant human interleukin-lbeta at 2.0 angstrom resolu A;Reference number: A44666; MUID:90064532; PMID:2585509
A;Filzel: Crystal structure, revystallography, 2.0 angstroms
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, ii, S.A.; Vinetskii, Y.P.
Johl. Akad. Nauk SSR 309.
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin A;Reference number: 138131; MUID:90249285; PMID:2635664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Algorited to the Brookhaven Protein Data Bank, January 1991
A; Reference number: A50049; PDB:611B
A; Reference number: A50049; PDB:611B
B; Contents: annotation; conformation by (13) C- and (1) H-NMR, residues 117-269
B; Cohemistry 30, 2315-2323, 1991
Biochemistry 30, 2315-2323, 1991
Biochemistry 30, 2315-2323, 1991
A; Title: High-resolution three-dimensional structure of interleukin lbeta in solution by A; Reference number: A44675; MUID:91159409; PMID:2001363
A; Contents: annotation; (1) H-NMR structural determination
B; Hazuda, D.J.; StrickLer, J.; Sinon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A; Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a con A; Reference number: A39774; MUID:91201363; PMID:2016316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2q13-2q21
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;117-269/Product: interleukin-1 beta #status experimental <1L1>
                                                                                                         S.; Hira
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>
A;Cross-references: GB:M54933; NII:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, Blochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: CDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A;Reference number: I52217; MUID:87156769; PMID:3493774
                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GDB:120094; OMIM:147720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: 138132
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <KOT>
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-269 <NIS>
```

ŝ

A;Cross-references: UNIPROT:P14628 R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, J. Immunol. 142, 2299-2306, 1989

```
Search completed: September 29, 2005, 11:17:33
Job time : 27.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rikerbhaw, J.
submitted to the EMBL Data Library, January 1996
submitted to the EMBL Data Library, January 1996
A; Reference number: 21993
A; References: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-425 < WIL>
A; Residues: 1-425 < WIL>
A; Cross-references: UNIPROT: Q22236; EMBL: Z68751; PIDN: CAA92974.1; GSPDB: GN00022; CESP: TO
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-268 < YOU>
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
C; Superfamily: interleukin-1
C; Keywords: Cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>
A,Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A,Reference number: A30584; MUID:89176242; PMID:2784458
                                                                                                                                              A;Residues: 1-268 cCAN>
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
B;Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and A;Reference number: A94230; MUID:89315718; PMID:2787507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 EKGSLIL-LGVSKGEFCL-YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIF-YRAQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 VKSLNPKKFSIHDQDHKVLVLDSGNLIAVPDKN--YIRPEIFFALASSLSSASAEKGSLI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 NFVHTSRKVKSLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 LIGVSKGEFCLYC--DKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNML 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T05E11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 NIDHEPGSVESQQSTIYSDSDDSPLDDE----VIPPKEQAMRKIEFALADIKRQMDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.4%; Score 86; DB 1; Length 268;
Best Local Similarity 24.8%; Pred. No. 2.4;
Matches 39; Conservative 29; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.4%; Score 85; DB 2; Length 425; Best Local Similarity 26.8%; Pred. No. 5.2; Matches 38; Conservative 18; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ESAQPPNWYISTSQTEYMPVFLGNNSGGQDLIDFSME 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 ESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:T05E11.4
A;Map position: 4
A;Introns: 16/3; 73/2; 151/3; 184/1; 260/1; 290/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 YGNOKYLDSSIKS---ICELLN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 VGSRNMLESAAHPGWFICTSCN 182
                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JU0082
                                                                          A; Accession: A30584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
```

e G

q δ

ઠે 셤 ò

Š

Ò,

g

ઠે a THE STATE OF THE S

```
129.5
129.5
129.5
127.5
123.5
123.1
123.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
121.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cluster."
                                                                                                                                                                                                                                                                       Q7RU00
                                                                                                                                                                                                                                               RESULT 1
Q7RU00
  mus musculu
h interleuk
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             шив шивсили
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h interleuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7ru00 homo sapien
Q9nzh6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tursiops tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyprinus ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equus cabal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sus scrofa
                                                                                        8; Search time 107 Seconds
(without alignments)
1043.302 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macaca
                                                                                                                                                                     1 MSFVGENSGVKMGSEDWEKD.....IEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9d6z6 m
Q9nzh8 b
Q7rtz9 b
Q9uha7 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099771
06uvx7 P
08r460 n
09j1a2 n
09ubh0 P
07rtz6 P
08cgal n
08r459 n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7rtz4 | P18510 | O77482 | P26890 | C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9gmz4
Q866r8
Q9beh0
Q29056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9nzh6
Q7rtz7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7rtz8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8wwz1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7rtz5
                15.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11F5 MOUSE
Q6UVX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILIX MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111X CANFA
111X PIG
11FA HUMAN
Q7RTZ5
111X RAT
111X HORSE
073909
                                                                                          September 29, 2005, 11:03:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIF6_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILIX BOVIN
ILIX RABIT
ILIX TURTR
Q866R8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11F8_MOUSE
11F9_HUMAN
Q7RTZ9
11F6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11F7 HUMAN Q7RT\overline{z}7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL1X HUMAN
                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1F9 MOUSE
                                                                  sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9DDF2
                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07RU00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBCGA1
                                                                                                                                                                                                                                                                                                                                                                           Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                 using
                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                                                               US-10-695-195-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152
178
159
177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                  protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
150
149.5
148.5
148.5
147.5
                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
155.5
155.5
153
151.5
                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
221
216.5
216.5
204
204
182.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
175.5
168
163.5
163.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1139.5
                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                     OM protein
                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٠
9
```

```
        32
        129.5
        11.2
        272
        2
        QBAXV9
        QBaxv9
        Carassius a QBaxv9 carassius a QT056

        34
        129
        11.2
        273
        2
        QFU03
        QCFU156
        Drachydanio QFU13

        34
        128.5
        11.1
        82
        2
        QGFU3
        QCFU13
        QCFU14
        Q
```

```
"Molecular cloning of the interleukin-1 gene cluster: construction of
an integrated YAC/PAC contig and a partial transcriptional map in the
region of chromosome 2q13.";
Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20545212; PubMed=11093146; MEDLINE=20545212; PubMed=11093146; DOI=10.1002/1552-4141(200011)30:11</br>
DOI=10.1002/1552-4141(200011)30:11
Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.; Barton J.L., Herbst R., Ecceptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."; Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=94245215; PubMed=8188271; Nicklin M.J.H., Weith A., Duff G.W.; Nicklin M.J.H., Weith A., Duff G.W.; a Physical map of the region encompassing the human interleukin-1-alpha, interleukin-1-beta and interleukin-1 receptor genes."; Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; Mulero J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanne R., Ford J.E.; Interleukin-1 receptor antagonist gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDINE-973126934; DOI=10.1006/geno.1997.4654; MEDILNE-97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654; Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Nothwang H.G., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.;
                                                                                                                                                                                                                                                      01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
IL-1F7b (IL-1H4, IL-1H, IL-1RP1).
                                                                                                                                                                                        219 AA
ALIGNMENTS
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 79:718-725(2002).
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kornman K.;
```

~

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sims J.E.;
                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11F7_HUMAN
                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yanaura D., Lewis L., Elgenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=21282953; PubWed=11278614; DOI=10.1074/jbc.M010095200; Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J., Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.; "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21359532; PubMed=11466363; Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S., Debets R., Timans J.C., Homey B., Zurawski S., Bazan J.P., Magner J., Edwards G., Clifford T., Menon S., Bazan J.P., Kastelein R.A.; Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q9QYYI; IMD6.
G0; G0:0005576; C:extracellular; IEA.
G0; G0:0005152; F:interleukin-1 receptor antagonist activity; IEA.
G0; G0:0006955; P:immune response; IEA.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR003297; InterleukinILIRA.
InterPro; IPR00975; Interleukin_1.
                                                                                                                                                                                                 MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
  MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                ur new members expand the interleukin-1 superfamily."; Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGM, PP00340; ILI; 1.
PRINTS; PR00264; INTERLEUKINI.
PRINTS; PR01360; INTELLEUKINI.
PPCODOM; PP002536; Interleukin 1; 1.
SEQUENCE 219 AA; 24242 MW; 18EBA0881DF25C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ber.";
Biol. Chem. 276:20597-20602(2001).
                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                      family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      interleukin-1
                                                                                                                                                                                                                                                                                              Young P.R.
                                                              Sims J.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lRrp.
                                                                                                                                                                                                                                                                                                                                                   the
  SOR BERRY BE
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLBSAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                             SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                              1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yansura D., Lewis L., Eigenbrot C., Henzl W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS B AND C), SEQUENCE OF 46-54, AND VARIANTS
                                                                                                                                                                                                                                                                                     MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ILL | THOMAN | STANDARD; | PRT; | 218 AA. |
| 218-FBB-2003 (Rel. 41, Created) | SPECIAL |
| 28-FBB-2003 (Rel. 41, Last sequence update) |
| 28-FBB-2003 (Rel. 44, Last annotation update) |
| 16-JUL-2004 (Rel. 44, Last annotation update) |
| 17-JUL-2004 (Rel. 44, Last annotation update) |
| 17-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and initial characterization of four novel members of
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM B).
TISSUB-Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;
MEDLINE-20209405; Pubmed-10744718; DOI-10.1074/jbc.275.14.10308;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.M.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS D AND E).
MEDIJNE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
"Genomic organization of the interleukin-1 locus.";
Genomics 79:726-733(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
     Length 219;
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Colon carcinoma;
Manoj P.P., Mantovani A., Muzio M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNCNEPVGVTDKFENRKHIEFSFQP-VCKAEMSPSEVSD 218
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    superfamily.";
                                                      Pred. No. 1.3e-92;
          Score 1139.5;
                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Four new members expand the IL-1 su
J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM B).
          98.7%;
99.1%;
                                                                                                                  Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1Rrp.";
Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAL-31 AND ALA-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HID THE SET OF THE SET
```

```
RX MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Alteshus R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteshul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Soderzen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Buterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Tand mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOID 29,09NZH6-5; Sequence=VSP 002655; TISSUE SPECIFICITY: Isoforms A, B and C are expressed in testis, colon, placenta, lung and lymph node. Isoforms D and E were found only in testis and bone marrow. Whereas only isoform A is found in brain, only isoform B in kidney and only isoform C in heart. INDUCTION: By phorbol ester (PMA) in different cell lines. SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds to interleukin-18 receptor (IL-18R) receptor but not to IL-1 receptor. Could be a new player in the inflammatory and immune responses mediated by the IL-18/IL-18R axis.
-!- SUBCELULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
[6]
SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ALA-42.
TISSUB=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM, 605510; -. Gratracellular; TAS. GG, GO:0005576; C:extracellular; TAS. GG, GO:00055149; F:interleukin-1 receptor binding; NAS. GG; GO:0006955; P:immune response; NAS. InterPro; IPR000995; Cytok Lil like. InterPro; IPR000975; Interleukin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event_Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9NZH6-2; Sequence=VSP_002653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9NZH6-3; Sequence=VSP_002656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=09NZH6-4; Sequence=VSP_002654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9NZH6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AP200496; AAF69252.1; --
EMBL, AF251188; AAG29344.1; --
EMBL, AF251181, AAG14420.1; --
EMBL, AF251120; AAG14422.1; --
EMBL, AF251120; AAG14422.1; --
EMBL, AF251139; AAG14421.1; --
EMBL, AF271840; AAL6712.1; --
EMBL; AY071841; AAL6715.1; --
EMBL; BC020637; AAH20637.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, BC020637; AAH20637.1;
HSSP, P18510; 11LR.
Genew, HGNC:15563; ILLF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H-InvDB; HIX0002387; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +
```

```
180
                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                     Interleukin 1 family member 7.
MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLP
                                                                                                                                                                                                      SPKVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                  1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                         SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIPFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPBIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                       isoform A).
/FIId=VSP 002653.
DPAGSPLEPGPSLPTWNFVHTS -> G (in isoform
                                                                                                           TMNFVHTS -> MSGCDRRETETKGKNSFKKRLRG
                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                            Score 1130; DB 1; Length 218;
Pred. No. 8.8e-92;
1; Mismatches 3; Indels (
        PRINTS; PRO0264; INTERLEUKINI.
SMART; SKOO2536; Interleukin_1; 1.
SMART; SKOO125; ILL; 1.
PROSITE; PSO0253; INTERLEUKIN 1; FALSE_NEG.
MALternative splicing; Cytokine; Direct protein sequencing;
Multigene family; Polymorphise; Removed in mature form.
                                                                                                                                                                                                                                                                          FTId=VAR_014261.
96E089310D2CEA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                               Missing (In isoform E) /FIId=VSP_002655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                   ົວ
                                                                                                                                                                                                           -> K (in isoform C
/FTId=VSP_002656.
G -> V
                                                                                                                                                                                                                                          3 -> V.
/FTId=VAR_014260.
                                                                                                                                                                       002654
                                                                                                                                                                     /FTId=VSP
                                                                                                                                                                                                                                                                    ٠. A.
                                                                                                                                                                                                                                                                                        218 AA; 24126 MW;
                                                                                                                                                                                                                                                                                                              97.8%;
98.2%;
                                                                                                                                                                                                                                                                                                                          al Similarity 98.2
214; Conservative
                                                                              45
218
49
                                                                                                                                                 49
                                                                                                                                                                                 88
                                                                                                                                                                                                        89
                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                 42
Pfam; PF00340; IL1; 1
                                                                                                                                                                                                                                                                 42
                                                                                                                                                 28
                                                                                                                                                                                 28
                                                                                                                                                                                                        49
                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                   VARSPLIC
                                                                                                                                                 VARSPLIC
                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                 VARIANT
                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
 ð
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

but

ö

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Last sequence update) Last annotation update) 157 AA Created) PRT; 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, PRELIMINARY; Homo sapiens (Human) IL-1F8 (FIL1-eta) NCBI\_TaxID=9606; O7RTZ7 RESULT 3

MEDLINE=20545212; PubMed=11093146;
DOI=10.1002/1521-4141(20011)30:11<2299::AID-IMMU3299>3.0.CO;2-S;
Barton J.L., Herbet R., Bosiato D., Higgins L., Nicklin M.J.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000). MEDIINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654; Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., SEQUENCE FROM N.A. SEQUENCE FROM N.A. 

```
176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I1F8
RATARAK KARAK KARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDT ACCO OC OC SERVER TO SERVER SERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J.,
Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
"Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                             "Molecular cloning of the interleukin-1 gene cluster: construction of
an integrated YAC/PAC contig and a partial transcriptional map in the
region of chromosome 2g13.";
Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                            MEDLINE=94245215; PubMed=8188271;
Nicklin M.J.H., Weith A., Duff G.W.;
"A Physical map of the region encompassing the human interleukin-1-
alpha, interleukin-1-beta and interleukin-1 receptor genes.";
Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-21988050; PubMed-11991722; DOI=10.1006/geno.2002.6751;
Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper B.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-20138623, PubMed=10860666; DOI=10.1006/geno.2000.6184;
Busfileld S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
Identification and gene organization of three novel members of th
IL-1 family on human chromosome 2.";
Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21359532; PubMed=11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; Mulero J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanner R., Ford J.E.; "ILIHY1: A novel interleukin-1 receptor antagonist gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Pour new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 276:20597-20602(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 79:718-725(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kornman K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cluster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sims J.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲
   RAHARAKA BARAHAN BARAHA BA
```

57 PKKFSIHDQDHKVLVLDLDSGNLIAVPDKNYIRPEIFFALA-SSLSSASAEKGSLILLGVSK 115 116 GEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGW 175 PKSYAIRDSROMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIKG Gaps "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, functic as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446."; Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI\_TaxID=10090; 4 STRAIN-Swiss Webster / NIH;
MEDLINE-2198051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
"Genomic organization of the interleukin-1 locus.";
Genomics 79:726-733(2002). Length 157; 50; Indels 20.3%; Score 234; DB 2; 34.8%; Pred. No. 1e-12; Q9D6Z6; Q8R461; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Interleukin I family member 8 (IL-IF8). Name=Illf8; Synonyms=Fille; Mus musculus (Mouse). 34; Mismatches 183 PRT; SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Tongue; FICTSCNCNEPVGVT 190 126 FIATSTISCOPIFLT 140 47; Conservative STANDARD; Query Match Best Local Similarity SEQUENCE FROM N.A. MOUSE

3;

169 AA.

PRT;

STANDARD;

HUMAN

```
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Na Nkaidon I., Oastro N., Saito R., Suzuki H., Yamanaka I., Kryosawa H.,
Yagi K., Tomaru Y., Hasegawa T., Nogami A., Schombach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Blake J.A., Bradpi A., Matsuda H., Baralov S., Beisell K.W.,
Blake J.A., Bradt D., Brusic V., Chorhia C., Corbani L.B., Cousins S.,
Blake J.A., Cariboldi M., Gissi C., Godzik A., Frazer K.S.,
Asasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Armanond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Angashima T., Numata K., Okido T., Pevra N., Pertea G., Pesole G.,
Rayasi T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Ravasi T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Bayashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Schneider C., Semple C.A., Setou M., Sakarun S.,
Ananai T., Wandhaw-Boris A., Yanagi I., Yang I., Yang I.,
Rayashima T., Wanghaw-Boris A., Yanagi I., Wang I.,
Rayashima T., Wanshaw-Boris A., Yanagi I., Wang I.,
Rayashima A., Hashizume W., Imotani R., Sakamura M., Sakaume N., Sakai K.,
Baninshi A., Yoshino W., Imotani K., Ishiata K., Shinagawa A.,
Baninshi A., Yoshino W., Imotani K., Ishiata K., Shinagawa A.,
Baninshi A., Yoshino W., Imacritone based on functional annotation of RT Go,770 full-length CDNAS.
Rayasunshi A., Yoshino W., Imacriptome based on functional annotation of RT G., The Wall-length CDNAS.
Rayasunshi A., Yoshino W., Imacriptome based on functional annotation of ST G., Sulland R., Shinagawa R., Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 IAVPDKNYIRPEIFFALA-SSLSSASAEKGSLILLGVSKGEFCLYCDKDKGQSHPSLQLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 POCCLEDPAGSPLEPGPSL----PTMNFVHTSRKVKSLNPKKFSIHDQDHKVLVLDSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 POSCVH------VLPPKSIQMWEPNHNTMHGS----SQSPRNYRVHDSQQMVWVLTGNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.1%; Score 221; DB 1; Length 183; 32.3%; Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 KEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Multigene family. SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY071842; AAL67152.1; ALT_INIT.
EMBL; AK009787; BAB26505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1916927; Illf8.
InterPro; IPR008996; Cytok ILl like.
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00340; IL1; 1.
PRINTS; PR00264; INTERLEUKIN1.
ProDom; PD002536; Interleukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00253; INTERLEUKIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01584; 1L2H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=2159532: PubMed=11466363; MEDLINE=2159532: PubMed=11466363; Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S., Magner J., Edwards G., Clifford T., Menon S., Bazan J.F., Kastelein R.A.; "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NP-kappa B activation through the orphan IL-1 receptor-related protein 2."; JIMMUNO1. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                              Young P.R.; "Identification and initial characterization of four novel members of
                                                                                 (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1 related protein 2)
                                                                                                                                                                                                                   TISSUE=Keratinocytes,
MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  (Interleukin-1 homolog 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis skin.
-!- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.
-!- SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0007267; P:cell-cell signaling; TAS.
GO:0009613; P:response to pest/pathogen/parasite; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FBB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 9 (IL-1F9) (Inter
                                                                                                                Name=IL1F9; Synonyms=IL1E, IL1H1, IL1RP2;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                          Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF200492; AAF69248.1; -. EMBL; AF206696; AAG35670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:15741; IL1F9.
                                                                                                                                                                                                                                                                                                             the interleukin-1 family.
                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Epithelium;
                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605542; -
                                                                                                   (IL-1RP2)
             9NZH8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
```

```
Sims J.E.;
[5]
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [12]
  4
                                                                                                                                                                                                                                                                                                     61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAE-KGSLILLGVSKGEFC 119
                                                                                                                                                                                                                                                                                                                                                                                                             120 LYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICT 179
                                                                                                                                                                                                                                                                                                                                             26 TINDINQOVWTLOGONLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13."; Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=2054512; PubMed=11093146;
MEDLINE=2054512; PubMed=11093146;
DDI=10.1002/1521-4141(200011)30:11<2299::AID-IMMU3299>3.0.CO;2-S;
Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1;
cluster lacks IL-1, IL-1ra, IL-1ra and IL-18 antagonist activities.";
ENT. J. Immunol. 30:2299-3308(2000).
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicklin M.J.H., Weith A., Duff G.W.; "A Physical map of the region encompassing the human interleukin-1-alpha, interleukin-1-beta and interleukin-1 receptor genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A sequence-based map of the nine genes of the human interleukin-1 cluster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           ر
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,
Hildebrandt F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
                                                                                                                                                                                                                18.7%; Score 216.5; DB 1; Length 169;
                                                                                                                                                                                                                                                           Indels
                                        Pfam; PF00340; IL1; 1.
PRINTS; PR00246; INTERLEUKINI.
SMART; SM00125; IL1; 1.
PROSTITE; SM00125; IL1; 1.
PROSTITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
CYCOKITE; MULTIGENE FARILY
SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                    ; Pred. No. 3.9e-11; 26; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-MAR-2004 (TrEMBLrel. 26, Created)
Ol-MAR-2004 (TrEMBLrel. 26, Last sequenc
Ol-MAR-2004 (TrEMBLrel. 26, Last annotat
IL-1F9 (IL-1H1, IL-1RP2, IL-1-epsilon).
  InterPro; IPR008996; Cytok_IL1_like.
                      interPro; IPR000975; Interleukin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94245215; PubMed=8188271;
                                                                                                                                                                                                                                       37.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SCNCNEPVGVTDK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::|::|
S-KRDQPIILTSE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 79:718-725(2002).
                                                                                                                                                                                                                                                           50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                  Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kornman K.;
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O7RTZ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
Q7RTZ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LID
DOT TO THE SERVICE SERVICE
  g
                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
SEQUENCE FROM N.A. MEDINE-21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200; Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J., Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.; "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=2106552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yangura D., Lewig L., Eigenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-21359532; PubMed=11466363; Debete R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S., Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F., Kastelein R.A.; Ifamily members, IL-1 delta and IL-1 epsilon, function "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor_related protein 2.J. Immunol. 167: 1440-1446.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young P.R.; "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.
GO; GO:0006955; P:immune response; IEA.
SEQUENCE FROM N.A.
MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; MIDLINE=99443727; Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.;
"ILHY1: A novel interleukin-1 receptor antagonist gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                       Four new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Der.";
Biol. Chem. 276:20597-20602(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-1 receptor-retactor process.
J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the interleukin-1 family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1Rrp.";
Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
```

```
Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                          Name=IL1F6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cluster."
                                                                                      Query Match
                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                 Q7RTZ8
O7RTZ8:
                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                     Q7RTZ8
                                                                                                                                                                                                                                                                                                                                               $ £ 8 8 8 8 8
                                                                                                                                                              욥
                                                                                                                                                                                        ઠે
                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                 119
                                                                                                                                                                                                                              LYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICT 179
                                                                                                                                                                                        85
                                                                                                                                                                                 26 TINDLNQQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: Binding analysis failed to detect interaction with multiple ILIR family members.
                                                                                                                                                                61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAE-KGSLILLGVSKGEFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Four new members expand the IL-1 superfamily.";
J. Biol. Chem. 275:1169-1175(2000).
-!- SUBCELLIULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: Expressed in immune system and fetal brain,
but not in other tissues tested or in multiple hematopoietic cell
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 6 (IL-1F6) (Interleukin-1 epsilon) (IL-1 epsilon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169; MEDLINE=20092888; Rubmad=10625660; Medlin M., Garka K.E., Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E., Sims J.E.;
                                                                                                               DB 2; Length 169;
                                                                                                                                        Indels
             InterPro; IPR003297; InterTeukInILRA.
InterPro; IPR003975; InterTeukInI.
Pfam; PP00340; ILI; 1.
PRINTS; PR00264; INTERLEUKINI.
PRINTS; PR01360; INTERLEUKINI.
PRINTS; PR01360; INTERLEUKINI.
PRODOM; P0002536; InterleukinI; 1.
SEQUENCE 169 Aa; 18721 MW; F00A9243706F4154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005149; F:interleukin-1 receptor binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR000975; Interleukin_1.
PR00340; IL1; 1.
                                                                                                            18.7%; Score 216.5; DB 2; 37.6%; Pred. No. 3.9e-11; tive 26; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                             158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
 Cytok ILL like.
InterleukinILIRA.
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=IL1F6; Synonyms=FIL1E, IL1E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF201831; AAF25211.1; -.
                                                                                                                                                                                                                                                                      180 SCNCNEPVGVTDK 192
                                                                                                                                                                                                                                                                                    | ::|::|
S-KRDQPIILTSE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01584; 1L2H.
Genew; HGNC:15562; IL1F6.
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
 IPR008996;
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602209
                                                                                                                                                                                                                                                                                                                                                         11F6 HUMAN
Q9UHA7;
                                                                                                                                           20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ines
  InterPro;
                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                               143
                                                                                                                Query Match
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                 11F6_HUMAN
                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                      ઠ
   8888888888
                                                                                                                                                                    ð
                                                                                                                                                                                          셤
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                              셤
```

```
4
                                                                                                                                                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 LILLGVSKGEFCLYCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNML 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 PIYLGLNGLANLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTF 118
                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13.";
                                                                                                                                                                                                                                                                                                                                                                    50 RKVKSLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGS
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20545212; PubMed=11093146;
DOI=10.1002/1521-414(200011)30:11<2299::AID-IMMU3299>3.0.C0;2-S;
Barton J.L., Herber R., Bosisio D., Higgins L., Nicklin M.J.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicklin M.J.H., Weith A., Duff G.W.;
"A Physical map of the region encompassing the human interleukin-1-alpha, interleukin-1-beta and interleukin-1 receptor genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654; Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.;
                                                                                                                                                                                                     Length 158;
                                                                                                                                                                                                                                                                     66; Indels
                                                                                                                         Cytokine; Multigene family.
SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                     17.7%; Score 204; DB 1;
35.1%; Pred. No. 4.6e-10;
tive 28; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 ESVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 ESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 AA
                         ProDom, PD002536; Interleukin_1; 1.
SMART; SM00125; ILJ; 1.
PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=94245215; PubMed=8188271;
PRINTS; PR00264; INTERLEUKIN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
IL-1F6 (FIL-1-epsilon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 79:718-725(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                        54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
```

```
MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J.,
Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
"Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799; Pan G., Risear P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E., Yansura D., Lewis L., Elembrot C., Henzel W.J., Vandlen R.; "IL-1H, an interleukin l'related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINES FROM N.A.

MEDLINES=1459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J., Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G., Pan Y., Smith D.E., Young P.R.;

Pan Y., Smith D.E., Young P.R.;

Trends Immunol. 22:536-537(2001).

-I- MISCELLANEOUS: The sequence shown here is derived from an EMBL/Genebank/DDBJ third party annotation (TPA) entry.

-I- SIMIL/Genebank/DDBJ third party annotation (TPA) entry.

-I- SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kastelein R.A.; "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antegorist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                     ō
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDIAGE 10860666; DOI=10.1006/geno.2000.6184; MEDIATRE=201318623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                 identification and initial characterization of four novel members the interleukin-1 family."; J Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                    MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21359532; PubMed=11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S., Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                         MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                     Drmanac R., Ford J.E.;
"ILLHY1: A novel interleukin-1 receptor antagonist gene.";
Biochem. Biophys. Res. Commun. 263:702-706(1999).
J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R
                                                                                                                                                                                       interleukin-1 superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0006954; P:inflammatory response; IEA.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR003294; InterleukInILIAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aber.";
Biol. Chem. 276:20597-20602(2001).
                                                                                                                                                                                                             Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                    Sims J.E.;
"Four new members expand the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QYY1; 1MD6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [9]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                               the
```

```
4
                                                                                                                                                                                                                                                                                                                                                                          62 PIYLGLNGLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEFV-KSFLFYHSQSGRNSTF 118
                                                                                                                                                                                                                                                                   50 RKVKSLNPKKPSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGS 107
                                                                                                                                                                                                                                                                                                                                                    108 LILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNML 167
                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=21359532; PubMed=11466363;

MEDLINE=21359532; PubMed=11466363;

MEDLINE=21359532; PubMed=11466363;

Magner J., Edwards G.C., Homey B., Zurawski S., Bazan J.R., Lo S.,

Kastelein R.A.; Edwards G., Clifford T., Menon S., Bazan J.F.,

Kastelein R.A.; Edwards G., Clifford T., Menon S., Bazan J.F.,

"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2.";

J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                            3 KALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090YI; 09JG2; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Interleukin 1 family member 5 (IL-IF5) (Interleukin-1 delta) (IL-1 delta) (Interleukin-1-like protein-1) (Interleukin-1-like protein 1) (IL-IL1) (Interleukin-1 homolog 3) (IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20545212; PubMed=11093146; DOI=10.1002/1521-4141(200011)30:11<-3299::AID-IMMU3299>3.0.CO;2-S; DOI=10.1002/1521-4141(200011)30:11<-3299::AID-IMMU3299>3.0.CO;2-S; Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.H.; "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."; Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINES-2009405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Stomach, and Tongue;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                 Score 204; DB 2; Length 158;
Pred. No. 4.6e-10;
                                                                                                                                                                                                                              66; Indels
                                                         PRINTS; PRO0264; INTERLEUKINI.
PRINTS; PR01359; INTRLEUKINIB.
PRINTS; PR01357; INTRLEUKNINB.
PRODOM; PD002536; Intexleukin_1; 1.
SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      168 ESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 ESVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AA
                                                                                                                                                                                                                              28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Illf5; Synonyms=Filld, Illh3, Illhy1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sinterleukin-1 family.";
Biol. Chem. 275:10308-10314(2000).
InterPro; IPR003296; InterleukinILlB.
              InterPro; IPR000975; Interleukin_1.
Pfam; PF00340; IL1; 1.
                                                                                                                                                                                      17.78;
                                                                                                                                                                                                         35.1%;
                                                                                                                                                                                                                              54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foung P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIFS MOUSE
                                                                                                                                               SEQUENCE
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIFS_MOUSE
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1H3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *****
                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                        ð
```

10 FRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEEISVVPNR------ALDASLSP--- 57

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    receptor-related protein 2-mediated response to interleukin 1
receptor-related protein 2-mediated response to interleukin 1
family member 9 (ILIF9). Could constitute part of an independent
signaling system analogous to interleukin-1 alpha (IL-1A), beta
(IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
IRI), that is present in epithelial barriers and takes part in
local inflammatory response (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
tissues containing epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%; Score 182.5; DB 1; Length 156; 34.5%; Pred. No. 3.6e-08; ive 21; Mismatches 37; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00125; ILL; 1.
PROSITE; PS00253; INTERLEUKIN 1; 1.
3D-Etructure; Cytokine; Multigene family.
2 2 Missing (in Ref. 3).
SEQUENCE 156 AA; 17136 MW; A4DIEE2P93CF77A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF230378; AAF91275.1; -.
EMBL, AK00974; BABZ6471.1; -.
EMBL, AX008977; BABZ6002.1; -.
EMBL, AJZ56429; CAB59831.1; ALT_INIT.
EMBL, AF200495; AAF69251.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002536; Interleukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00340; IL1; 1.
PRINTS; PR00264; INTERLEUKIN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1MD6; X-ray; A=3-156.
MGD; MGI:1859325; Illf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

```
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 KGSLILLIGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSR 164
104 EKGSLILLGVSKGEFCLYCDXDXGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVG 162
                    effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13.2265-2270(2003).
-!- SIMILARITY: Belongs to the IL-1 family.
EMBL, AV353111; AAQ89469.1; -.. GO, GO:0005575; C:extracellular: IRA.
GO, GO:0005575; P:interleukin-1 receptor antagonist activity; IRA.
GO; GO:0005955; P:immune response; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dowd P.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22887296; PubMed=12875309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P. Batton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SPDI), a large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
15.7%; Score 181; DB 2; Length 134;
Best Local Similarity 44.3%; Pred. No. 4e-08;
Matches 39; Conservative 17; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 AA; 14928 MW; D5369C5AD44A9752 CRC64;
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The secreted protein discovery initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : ||| | | | || :| ::|: :| :
STLESVAFPDWFIASS-KRDQPIILTSE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 NMLESAAHPGWFICTSCNCNEPVGVTDK 192
                                                                       163 SRNMLESAAHPGWFICTSCNCNEPVGVT 190
                                                                                            : ||||:||||:|||| ::|| :|
108 LTSSFESAAYPGWFLCTSPEADQPVRLT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008996; Cytok II like.
InterPro; IPR003297; InterTeukIniliRA.
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00264; INTERLEUKINI.
PRINTS; PR01360; INTRLEUKINIX.
ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; IL1; 1.
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                ORFNames=UNQ2456;
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
11F9_MOUSE
1D 11F9 MOUSE
AC QRR460;
DT 28-FEB-2003 (1)
DT 28-FEB-2003 (2)
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                         28
                                                                                                                                                                 RESULT 10
                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                     셤
                                                                             à
                                                                                                             용
   ઠે
```

51; Conservative

Best Local Similarity Matches 51; Conserv

39;

```
Young
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 IHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSL-SSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                     VPDLDQQVWIFRNQALVTVPRSHRVTPVSVTILPCKYPESLEQDKGIAIYLGIQNPDKCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 6 (LL-1F6) (Interleukin-1 epsilon) (IL-1
epsilon) (FIL1 epsilon) (Interleukin-1 homolog 1) (IL-1H1).
Name-Illf6; Synonyme-Fille, Ille, Illh1;
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                   SEQUENCE FROM N.A.
STRAIN=Swiss Webster / NIH;
MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
"Genomic organization of the interleukin-1 locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
Cytokine; Multigene family.
SEQUENCE 164 AA; 18733 MW; A7338D475DFEADBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 175.5; DB 1
31.7%; Pred. No. 1.6e-07;
ive 26; Mismatches 66
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 9 (IL-1F9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 AA.
                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:2449929; I11f9.
InterPro; IPR008996; Cytok ILL like.
InterPro; IPR000975; Interleukin 1.
                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00264; INTERLEUKINI.
ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; ILI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CNCNEPVGVTDKFENRKHIEFS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 KTGN-PIFLTSKKGEYYNINFN 159
                                                                                                                                                                                                                                                                                                                                         EMBL; AY071843; AAL67153.1; -. HSSP; P01584; 1L2H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 31.7% Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00340; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                               Mus musculus (Mouse)
                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9JLA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRECTION
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
RE SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

STRAIN=C3781663; PubMed=12466651; DOI=10.1038/nature01266;

REDINE=22354683; PubMed=12466651; DOI=10.1038/nature01266;

RA OKAZARI Y., Puturo M., Kasukawa T., Adachi J., Kananaka H., Kiyosawa H., Nikaido I., Osato N., Saitor R., Suzuki H., Yamanaka T., Kiyosawa H., Nikaido I., Osato N., Saitor R., Suzuki H., Yamanaka T., Colbach J., Colobori T., Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriffl L.M., Kananin A., Matsuda H., Batalov S., Beisel K.W., Dalla E., Dragami T.A., Pletcher C.F., Forrest A., Frazer K.S., Anai A., Kawaji H., Rawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Jackson I.J., Jarvis E.D., Ranai A., Kawaji H., Marchin I.V., Lee Y., Lenhard B., Lyons P.A., Rapitte R., Pontius J.U., Old. P., Ramachandran S., Rapasaka R., Pontius J.U., Old. P., Ramachandran S., Rayasai I., Marchin I.V., Reed J.C., Reed J.U., Reid J. W., Reimachandran S., Ravasi T., Reed J.C., Reed J.U., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setou M., Sakazune N., Sato K., Hingara R., Takenaka Y., Yang I., And J., Alizawa K., Alakawa T., Phkuda S., Harcane-Kishikawa T., Runnin M., Materston M., Sakazune N., Sakai K., Sasaki D., Shibata K., Shibata K., Shanisha A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Mature 420:563-573 (2002).

Rangure A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Mature 420:563-573 (2002).

Rangure A., Hashizume W., Materston R., Lander E.S., Rogers J., Rangure A., Hashisum R., Tanger E., Romana I., Shibata K., Sakai K., Sasaki D., Shibata K., Shibata 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                 oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function
                                                                                                                                                                                                                                                                                                                                                                                 "Identification and initial characterization of four novel members
                                                                                                                                                                                                                                       Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, funct
as an antagonist and agonist of NF-kappa B activation through the
orphan IL-1 receptor-related protein 2.";
J. Immunol. 167:1440-1446(2001)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                 MEDLINE-20209405; PubMed-10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zurawski S., Sana T.R., Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21359532; PubMed=11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R.,
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple ILIR family members. SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                        the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF200493; AAF69249.1; -. EMBL; AF206697; AAG35671.1; -. EMBL; AX004061; BAB23147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF206697; AAG
EMBL; AK004061; BAB
HSSP; P01584; 1HIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                              SEQUENCE FROM N.A.
                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kastelein R.A.;
```

```
Debets |
  46 VHTSRKVKSLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFAL-ASSLSSASAE 104
                                                                                                                                                                                                                   KGSLILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSR 164
                                                                                                                                                                                                                                       61 RGDPTYMGVQRPMSCLFCTKDGEQ--PVLQLGEGNIMEMYNKKEPVKAS-LFYHKKSGTT 117
                                                                                                                                                                                            9
                                                                                                                                                                                     DOI=10.1002/1521-4141(200011)30:11-3299::AID-IMMU3299>3.0.CO;2-8; Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.H.; "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-18, IL-18 and IL-18 antagonist activities:"; Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1L)
delta) (FILI delta) (Interleukin-1-like protein 1) (IL-1L)
homolog 1) (IL-1HY1) (IL-1HY1) (IL-1HY1) (IL-1 related protein 3) (IL-1RP3)
(UNQ1895/PRO4342).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=ILIFS; Synonyms=FILID, ILIHYI, ILILI, ILIRP3;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal skin;
MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
Drmanac R., Ford J.E.;
"ILHIY1: a novel interleukin-1 receptor antagonist gene.";
Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                  64; Indels
                                                                                         Cytokine, Multigene family. – SEQUENCE 160 Aa; 18015 MW; AA0434D68FF62F4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    superfamily.";
                                                                                                                            14.5%; Score 168; DB 1; 29.8%; Pred. No. 7.1e-07;
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                              155 AA
                                                                               PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
MGD; MGI:1859324; Illf6.
InterPro; IPR008996; Cytok ILl like.
InterPro; IPR000975; Interleukin_1.
Pfam; PP00340; ILL; 1.
                                           PRINTS; PRO0264; INTERLEUKINI.
ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; IL1; 1.
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    our new members expand the IL-1 Biol. Chem. 275:1169-1175(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20545212; PubMed=11093146;
                                                                                                                                                                                                                                                                165 NMLESAAHPGWFI -- CTSCNC 183
                                                                                                                                                                                                                                                                                      118 STFESAAFPGWFIAVCSKGSC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21359532; PubMed=11466363;
                                                                                                                                                 29;
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                               ILPS HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sime J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Four new
                                                                                                                                                                                                                     105
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                   ILFS HUMAN
                                                                                                                                                  datches
                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                          ઠ
```

```
Debets R. Tiennal JC., Norway B., Zurwawki S., Baran JR., D S., Rastelain R.A., Wagner J. T., Edwards G., Clifford T., Menon S., Baran JR., D S., Rastelain R.A., Wagner J. T., Edwards G., Clifford T., Menon S., Baran JR., D S., Rastelain R.A., Maratelain R.A.,
```

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send a mail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SLILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 SLSPVILGVQGGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 FRMKDSALKVLYLHNNQL------LAGGLHAGKVIKGEEISVVPNRWLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20545212; PubMed=11093146;
DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
Barton J.L., Herber R., Boalsio D., Higgins L., Nicklin M.J.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005152; F:interleukin-1 receptor antagonist activity; TAS. InterPro; IPR008996; Cytok IL1 like. InterPro; IPR008975; InterTeukīn_1. PF00910; IL1; I. FP00810; IL1; I. FP00810; IL1; I. FP00810; IL1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,
Hildebrandt F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.2%; Score 163.5; DB 1; Length 155; 32.9%; Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Created)
WARR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
IL-1F5 (IL-1HY1, FIL1-delta, IL-1RP3, IL-1L1, IL-1-delta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 FSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00264; INTERLEUKINI.
ProDom; PD002536; Interleukin_1; 1.
SWART; SM0125; IL1; 1.
PROSITE; PS00253; INTERLEUKIN_1; 1.
CYCOKINE; Multigene family.
SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 RNMLESAAHPGWFICTSCNCNEPVGVTDKFEN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : {||||:||||:||
TSSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 1.7e-
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                       EMBL, AF201830, AAF25210.1, --
EMBL, AF186094, AAF02757.1, --
EMBL, AJ242737, CAB59822.1, --
EMBL, AJ242738, CAB59823.1, --
EMBL, AJ271338, CAB67704.1, --
EMBL, AF216693, AAF7681.1, --
EMBL, AF230377, AAF91274.1, --
EMBL, AF350117, AAG9475.1, --
EMBL, BC024747, AAH24747.1, --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 50; Conservative
                                                                                                                                                                                                                                                                                                                             HGNC:15561; IL1F5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                              PIR; JC7104; JC7104.
HSSP; P18510; 11LR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                    MIM; 605507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7RTZ6
                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .∂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

```
SEQUENCE FROM N.A.
MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yansura D., Lewis L., Bigenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
Lin H.S., Ho A.S., Halbey-Vicente D., Zhang J., Bernal-Fussel J.,
Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
"Cloning and characterization of IL-1HY2, a novel interleukin-1 family
"Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13."; Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
                                                                                                     SEQUENCE FROM N.A.
MEDLINE=94245215; PubMed=8188271;
Nicklin M.J.H., Weith A., Duff G.W.;
"A Physical pot the region encompassing the human interleukin-1-
alpha, interleukin-1-beta and interleukin-1 receptor genes.";
Genomics 19:382-384(1994).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                            A sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BUBLINE-2018623 BLOMEd=10860666, DOI=10.1006/geno.2000.6184;
Busfiteld S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
Identification and gene organization of three novel members of t)
Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; Malter J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.;
ILIHY1: A novel interleukin-1 receptor antagonist gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21359532; PubMed=11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Four new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin-1 family.";
Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ber.";
Biol. Chem. 276:20597-20602(2001)
                                                                                                                                                                                                                                                                                                                                                                 Genomics 79:718-725(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kastelein R.A.;
                                                                                                                                                                                                                                                                                                             Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sims J.E.;
                                                                                                                                                                                                                                                                                                                                                   cluster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1Rrp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
```

SO DRANGE OF REAL STREET OF STREET O

```
Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
           SOW WHEN THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                             MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; SEQUENCE FROM N.A.

SEQUENCE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; Sina J.B., Nicchin M.J., Bazan J.F., Barton J.L., Busfield S.J., Sana J.B., Nicchin M.J., Rateleian R.J., Kunar S., Lin H., Mulero J.J., Pan G., A. Pord J.B., Xoung P.R.; Pan Fow nomenclature for the IL-1-family genes."; Trends Immunol. 22:536-537(2001).

TRENDS IMMUNOL CAD29877.1; The sequence shown here is derived from an EMBL/GenBank/DBD third party annotation (TPA) entry.

EMBL/GenBank/DBD third party annotation (TPA) entry.

EMBL/GenBank/DBD third party annotation (TPA) entry.

EMBL, EN000002; CAD29877.1; The Sequence shown here is derived from an GO; GO:0005956; C:extracellular; IEA.

GO; GO:0005956; C:extracellular; IEA.

GO; GO:0005956; C:extracellular; IEA.

GO; GO:0005956; C:extracellular; IEA.

InterPro: IPR003296; InterleukinILIB.

InterPro: IPR003296; InterleukinILIRA.

PRINTS; PR00340; ILI; 1.

PRINTS; PR00340; ILI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 SLSPVILGVQGGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVB/N; TISSUE=Mammary tumor; STRAIN=FVB/N; TISSUE=Mammary tumor; STRAIN=22380557; Dubmed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 --SLILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446."; J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.2%; Score 163.5; DB 2; Length 155; 32.9%; Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 FSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002536; Interleukin 1; 1.
PROSITE; PS00253; INTERLEUKIN 1; UNKNOWN 1.
SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||||:|||:||| : || || : || 139
108 TSSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 RNMLESAAHPGWFICTSCNCNEPVGVTDKFEN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin 1 receptor antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBCGA1
QBCGA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
```

δ 쉽 δ d

셤

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 CLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFIC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 CLSCAKSGDDI--KLÓLBEVNITDLSKNKEEDKR-FTFIRSEKGPTTSFESAACPGWFLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
60 FSIHDQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSSASAEKGSLILLGVSKGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 FRIWDTNQKTFYLRNNQLIA----GYLQGPNI--KLEBKLDMVPIDLHS-VFLGIHGGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=FUB/N; TISSUB=Mammary tumor;
Straubberg N.;
Straubberg (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-i- ShinLaRITY: Belongs to the IL-1 family.
EMBL; BC042532; AAH42532.1; --
HSSP; P18510; ILLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 159 AA; 17995 MW; BCA081C172903367 CRC64;
                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%; Score 162; DB 2;
33.3%; Pred. No. 2.4e-06;
tive 22; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 29, 2005, 11:16:36
Job time : 109 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:96547; Illrn.
GO; GO:0030073; P:insulin secretion; IMP.
GO; GO:0006629; P:insulin secretion; IMP.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR008297; InterleukinIilRA.
InterPro; IPR00927; InterleukinIilRA.
Pfam; PP00340; ILI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 TSCNCNEPVGVTDKFENRKHI-EFSFQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0264; INTERLEUKINI.
PRINTS; PR01360; INTRLEUKINIX.
ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; ILI!; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00253; INTERLEUKIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 33.3
Matches 49; Conservative
```

THIS PROF BLANK USERO

Sequence 6, A Sequence 11, Sequence 6, Ap Sequence 7, A Sequence 4

Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 25, Appli Sequence 25, Appl Sequence 11, Appl Sequence 142, Appl

4 US-10-788-963-6
4 US-10-302-554-7
6 US-09-876-790-9
7 US-10-888-918-9
7 US-10-888-918-9
7 US-10-888-780-9
7 US-10-888-931-9
7 US-10-965-528-25
8 US-10-065-964-25
8 US-10-063-541-142
8 US-10-063-551-142
8 US-10-063-551-142
8 US-10-063-551-142

ĕ

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
PILING DATE: 17-589-1999
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 496-1200
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
11116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
1116
116
116
116
116
116
116
116
116
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
  Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
                                                                                                                                                              September 29, 2005, 11:10:54 ; Search time 118 Seconds
(without alignments)
766.909 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/9CT_NEW PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
                                                                                                                                                                                                                                                         US-10-695-195-2
1155
1 MSFVGENSGVKMGSEDWEKD.....IEFSFQPVCKAEMSPSEVSD
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-788-963-2

1 US-10-139-833-12

1 US-10-302-554-12

1 US-10-302-554-14

1 US-10-876-790-8

1 US-10-888-918-8

1 US-10-888-780-8

1 US-10-888-780-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-695-195-2
US-10-694-978-2
                                                                                                                                                                                                                                                                                                                                                                                                                          1846076 seqs, 415116000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.8
97.8
97.8
97.8
97.5
97.1
97.1
97.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1155
1130
1130
1130
1120
1121
1121
1121
                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                          protein
                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

US-10-227-693-142 US-10-063-563-142 US-10-063-555-142

ALIGNMENTS

```
Length 218;
                                                                                                                                                                                                                                                                                                             CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                           181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
100.0%; Score 1155; DB 15;
100.0%; Pred. No. 9.2e-115;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1130; DB 9;
Pred. No. 4.3e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/10139833; Publication No. US20030004106A1; GENERAL INFORMATION: APPLICANT: Saris, Christiaan M. APPLICANT: Giles, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.8%;
Best Local Similarity 98.2%;
Matches 214; Conservative 1
                   Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 218
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-139-833-12
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-788-963-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-788-963-2
                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                        61
                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
   Query Match
                                                                                                               셤
                                                                                                                                                      ð
                                                                                                                                                                                          셤
                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10694978
Publication No. US20040087766A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                              121 YCDXDXGQSHPSLQLKKEKLMXLAAQXESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                        YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                   1 MSFVGENSGVKMGSEDWEKDEPOCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                ö
                                                                                                                                                                      ; Score 1155; DB 15; Length 218; Pred. No. 9.2e-115; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNCNEPVGVIDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNCNEPVGVTDKFENRKHIEFSFOPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/99,398,412
FILING DATE: 17-Sep-199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DX0904K TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-694-978-2
                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-695-195-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 218 amino acids TYPE: amino acid
                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-10-694-978-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                               ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                        1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSPKVKNINPKKF
                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
             Gaps
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09788963
Sequence 2, Application US/09788963
GENERAL No. US2002002473A1
GENERAL INFORMATION:
APPLICANT: YOUNG, PETER R.
APPLICANT: KUMAR, SANJAY.
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
FILE REFERENCE: GP-70607-1C1
CURRENT APPLICATION NUMBER: US/09/788,963
CURRENT FILNG DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR PRIOR PRIOR OFFER PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
```

Pred. No. 4.3e-112;

98.2%;

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09-876-790-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                               셤
                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                         ð
                                                                                                                                                                                                                          ò
                   APPLICANT: Xia, Min.
APPLICANT: Xia, Min.
APPLICANT: Ass, Min.
APPLICANT: Bas, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APLICANT: Graveiro, Roger
TITLE OF INVENTION: Uses Thereof
FILE OF INVENTION: Uses Thereof
FILE REPERBUCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT APPLICATION NUMBER: US/10/139,833
FILE REPERBUCE: 2002-05-06
FRIOR APPLICATION NUMBER: 60/170,191
FRIOR PILING DATE: 1999-12-10
FRIOR PILING DATE: 2000-03-09
FRIOR PILING DATE: 2000-04-04
FRIOR PILING DATE: 2000-04-04
FRIOR PILING DATE: 2000-04-04
FRIOR APPLICATION NUMBER: 60/195,910
FRIOR APPLICATION NUMBER: 60/195,910
FRIOR APPLICATION NUMBER: 09/724,583
FRIOR APPLICATION NUMBER: 09/724,583
FRIOR APPLICATION NUMBER: 09/724,583
FRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ 1D NOS: 37
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10302554
; Bequence 2, Application US/10302554
; Publication No. US20030148467A1
; GENERAL INFORMATION:
    APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: BeFERENCE: 1NTERLEUKIN-1 HOMOLOG ZILIA4
; TILE REFERENCE: 98-59
CURRENT APPLICATION NUMBER: US/10/302,554
; CURRENT FILING DATE: 1999-10-27
; PRIOR FILING DATE: 1999-10-27
; PRIOR FILING DATE: 1998-10-27
; WINDER APPLICATION NUMBER: US 60/105,824
; WINDER APPLICATION NUMBER: US 60/105,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1130; DB 14;
Pred. No. 4.3e-112;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 214; Conservative
      Sharon X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-10-139-833-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

97.8%; Score 1130;

Query Match

```
ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSRKVKSLNPKKF
                                    1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10302554

publication No. US20030148467A1

GENERAL INPORMATION:
APPLICANT: West, Robert R.
APPLICANT: West, Robert R.
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZILIA4
FILE REFERENCE: 98-59
CURRENT APPLICATION UNMBER: US/10/302,554
CURRENT APPLICATION NUMBER: US/09/428,118
PRIOR FILING DATE: 2002-11-22
PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 14

LENTETT: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.5%; Score 1126; DB 14; Best Local Similarity 97.7%; Pred. No. 1.2e-111; Matches 213; Conservative 2; Mismatches 3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: variant protein US-10-302-554-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09876790; Publication No. US20030091532A1; GENERAL INFORMATION: APPLICANT: SIMS, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
    Matches 214; Conservative
```

```
APPLICANT: SIMS, John E.
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, TEL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPT TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPT FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888,867
CURRENT FILING DATE: 2004-07-09
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR PILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHIL VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SIHDQDHKVLVLDDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                          61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                        121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1121; DB 17; Length
Pred. No. 4e-111;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                          CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/10888779; Publication No. US20050009138A1; GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/1088867; Publication No. US20050009075A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.1%;
Best Local Similarity 97.7%;
Matches 213; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-888-779-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-888-867-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 8
                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                    g
                                                                                                                                                                          ò
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/1088918;
Publication No. US20040248187A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SIMS, John E.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND KRECZ DNAS AND POLYPEPTI FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888,918
CURRENT APPLICATION NUMBER: US/209/876,790
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-12-14
SOFTWARE: PRIOR TILING DATE: 1999-12-14
SOFTWARE: PRIOR PLING DATE: 1999-12-14
SOFTWARE: PATOR PLING DATE: 1999-12-14
SOFTWARE: PATOR PLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 8
LUMBER OF SEQ ID NOS: 15
SEQ ID NO 8
LUMBER OF SEQ ID NOS: 15
APPLICANT: SMITH, Dirk B.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPT]
FILE REPERENCE: 2000-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.1%; Score 1121; DB 16; Best Local Similarity 97.7%; Pred. No. 4e-111; Matches 213; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.1%; Score 1121; DB 10;
Best Local Similarity 97.7%; Pred. No. 4e-111;
Matches 213; Conservative 1; Mismatches 4;
                                                                             FILE KEFERENET 2009-US
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 06/112,163
PRIOR FILING DATE: 1990-12-14
PRIOR FILING DATE: 1990-12-14
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCH IN VERSION 3.1
SOFTWARE: PATCH IN VERSION 3.1
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-09-876-790-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: H
US-10-888-918-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca.
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       염.
```

```
# APPLICANT: SIMS, John E.
# APPLICANT: BORN, Teresa L.
# TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPT FILE REFERENCE: 2008-US
# CURRENT APPLICATION NUMBER: US/10/888,931
# CURRENT APPLICATION NUMBER: US/09/876,790
# PRIOR APPLICATION NUMBER: 60/112,163
# PRIOR PILING DATE: 1999-11-10
# PRIOR APPLICATION NUMBER: 60/112,163
# PRIOR APPLICATION NUMBER: 60/112,163
# PRIOR PILING DATE: 1999-11-10
# PRIOR PILING DATE: 1999-11-10
# PRIOR PILING DATE: 1999-11-10
# PRIOR FILING DATE: 1999-12-14
# NUMBER: OF SEQ ID NOS: 15
# NUMBER: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                       61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                               YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 1121; DB 17;
97.7%; Pred. No. 4e-111;
tive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10695195
Publication No. US20040068099A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
                                                                                                                                                                                                                                                                                                                                                                 US-10-888-931-8
; Sequence 8, Application US/1088931
; Publication No. US20050013798A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 97.7
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-888-931-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-695-195-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                      181
                                                                                            61
                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                          g
                                              g
                                                                                          ò
                                                                                                                       g
                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                  ò
                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SIMS, John B.
APPLICANT: SIMS, John B.
APPLICANT: SIMS, John B.
APPLICANT: SIMS, John B.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPTI FILE REPERBUCE: 2008-US
CURRENT PILING DATE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
PRIOR APPLICATION NUMBER: US/09/876,790
PRIOR PELING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-12-14
SPRIOR FILING DATE: 1999-12-14
SOFTWARE: PARCHILING DATE: 1999-12-14
SOFTWARE: PARCHILING DATE: 1999-12-14
APPLICANT: BORN, Teresa L.

TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPTI FILE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPTI STLEE SOOG-US
CURRENT APPLICATION NUMBER: US/10/888,779
CURRENT FILING DATE: 2004-07-09
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-112-14
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFVGENSGVRAGSEDWEKDEPQCCLEDPAVSPLEPGPSLPTMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 1121; DB 17; Length 218; Pred. No. 4e-111; 1; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNCNE PVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1121; DB 17;
Pred. No. 4e-111;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 8, Application US/10889780; Publication No. US20050013797A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.7%;
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.1%;
Best Local Similarity 97.7%;
Matches 213; Conservative
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-10-888-779-8
                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-888-780-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-888-780-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>Ş</u>,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

```
Sequence 6, Application US/10679201

Sequence 6, Application US/10679201

Bublication No. US20040120923A1

GENERAL INFORMATION:

APPLICANT: DINNEELLO, CHARLES A.

APPLICANT: BUFLER, PHILIP

TITLE OF INVENTION: IL-18BP TO INHIBIT THE ACTIVITY OF A SECOND CYTOKINE

TITLE OF INVENTION: IL-18BP TO INHIBIT THE ACTIVITY OF A SECOND CYTOKINE

TITLE OF INVENTION: IL-18BP TO INHIBIT THE ACTIVITY OF A SECOND CYTOKINE

CURRENT APPLICATION NUMBER: US/10/679,201

CURRENT APPLICATION NUMBER: 60/416,827

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 3.2

LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                               COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1116; DB 15;
Pred. No. 1.4e-110;
1; Mismatches 5;
                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-0ct-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.6%; Score 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.6%;
     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rypE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.2
Matches 212, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-679-201-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-694-978-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10694978
Sequence 4, Application US/10694978
Publication No. US20040087766A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: DANK Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STRATE: California
COUNTRY: USA
TITLE OF INVENTION: Mammalian Cytokines, Related Reagents and Methods NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSRNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
                                                                                                                                             STATE: California
COUNTRY: USA

ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THE PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/10/695,195
FILING DATE: 27-OCC-2003
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNCNEPVGVTDKFENRKHIEFSFOPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.6%; Score 1116; DB 15; Best Local Similarity 97.2%; Pred. No. 1.4e-110; Matches 212; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17.5ep-199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQ ID NO: 4: US-10-695-195-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
```

ð 셤 ઠ 셤 ò 셤 ò g

ó

Gaps

; 0

```
ó
                                     0; Gaps
Best Local Similarity 97.2%; Pred. No. 1.4e-110;
Matches 212; Conservative 1; Mismatches 5; Indels
                                                                                  Search completed: September 29, 2005, 11:22:40 Job time : 119 secs
                          g
                                       à
                                               g
                                                                       g
                 ò
                                                         ઠે
                                                                                   δ
                                                                                            g
```

Н

```
8; Search time 65.5 Seconds (without alignments) 1287.233 Million cell updates/sec
                                                                                                                                                                                                       US-10-695-195-4
1165
1 MSFVGENSGVKMGSEDWEKD.....IEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                 2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        2105692 seqs, 386760381 residues
                                                                                                                       September 29, 2005, 10:55:38
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                      Sequence:
                                                                                                                             Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq\_16Dec04:\*

1. geneseqp1980s:\*
2. geneseqp1980s:\*
3. geneseqp2001s:\*
5. geneseqp2001s:\*
6. geneseqp203as:\*
7. geneseqp2003as:\*
8. geneseqp2003bs:\* 2 6 4 6 6 6 8 Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay91885 Primate i	Aab47186 IL-1 rela	Aag68116 Human int	Adj88306 Human int	-	Adn41836 Amino aci	Ado04679 Human int	9 Human	Aay70927 Human zil	Aay96940 Human IL-	Aab28266 Human int	6	Adn05012 Antipsori		Adh89067 Human zil	3 Human	Adh89075 Human zil	Aay70931 Human zil	Adh89072 Human zil	Aay91884 Primate i	Adj88304 Human int	Adl15866 Human int	Ado04677 Human int	Aay96938 Human IL-	Aab85138 Interleuk
			7	~	~	~	~	7	~	~	7	_	_	_	7	7	_	_	_	_	_	_	_	_	_	_
SUMMARIES	ID	AAY91885	AAB47186	AAG68116	ADJ88306	ADL15868	ADN41836	AD004679	AAY95299	AAY70927	AAY96940	AAB28266	AAB85136	ADN05012	AAY71084	ADH89067	AAY70933	ADH89075	AAY70931	ADH89072	AAY91884	ADJ88304	ADL15866	AD004677	AAY96938	AAB85138
	DB	٣	4	4	æ	60	œ	ω	m	m	m	ო	4	œ	m	7	ო	7	m	7	m	80	œ	œ	m	4
	Length	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	207	198
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.7	99.1	99.1	99.1	99.1	99.1	æ	98.8	98.7	98.7	97.7	7.76	95.8	95.8	95.8	95.8	95.3	89.8
	Score	1165	1165	1165	1165	1165	1165	1165	1161	1154	1154	1154	1154	1154	1151	1151	1150	1150	1138	1138	1116	1116	1116	1116	1110	1046
	Result No.	-	8	m	4	5	9	7	σ,	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

WO200017363-A2

30-MAR-2000.

218 3 AAY70928 218 7 ADH89068 1197 3 AAY89300 1176 8 ADL66905 1178 2 AAW93057 1178 2 AAW93057 1192 3 AAY95297 1193 3 AAY96934 1193 4 AAB87596 1193 5 ABG95921 1193 6 ABU72022 1193 6 ABU72022	Aay70928 Human zil Adh8968 Human zil Aay95300 Human int Aab48081 Human ext	10000	- 8	Novel Human Novel Human	Abu91030 Human PKO Abo27351 Human sec Abu92546 Human sec Abu81216 Human sec
	AAY70928 ADH89068 AAY95300 AAR8081	ADL66905 AAW93057 AAX95297 ADN05880	AAY96933 AAY96934 AABB7596 ABG95921	ABU90946 ABO34005 ABU72022 ABU71576	ABU91030 ABO27351 ABU92546 ABU81216
	118 3 118 7 197 3	776 78 92 92 92 93	93 3 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		
	1034 1034 1026.5	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	895 885.5 885.5	885.5 885.5 885.5	888 885 885 885 885 885 885 885 885
1034 1034 1034 1034 1034 919 919 919 919 919 919 919 919 919 91	225 28 28	, O H O E	66 8 8 8 4 8 6 7 6 9 7 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9	38 39 40 11	4 4 4 4 2 6 4 7

S
22
-
=
ш
Σ.
z
řή
ĭ
-

AAY91885 standard; protein; 218 AA.

RESULT 1 AAY91885

```
100. .106 _ _ _ vhich is part of a primary binding segment to the IL-1 receptor type"
                                                   Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
hypoglycemia; plasma iron; plasma zinc; acute liver response;
plasma copper.
                                         Primate interleukin-1 like molecule (IL-1-zeta) alternative Bequence
                                                                                                                                                                                                                                                                               /label= beta_strand_10
185. 204
/label= beta_strand_11
201. 204
/label= beta_strand_12
                                                                                                                                                                                                                           54. .161
|Jabel= beta_strand_8
                                                                                                              58. .64
/label= beta_strand_1
                                                                                                                            69. .74
/label= beta_strand_2
                                                                                                                                          6. .80
label- beta_strand_3
                                                                                                                                                        91. 96
/label= beta_strand_4
                                                                                                                                                                                                      'label = beta_strand_5
                                                                                                                                                                                                             18. 126
|abel= beta_strand_6
                                                                                                                                                                                                                                                                  beta_strand_9
                                                                                                    cocation/Qualifiers
                            (first entry)
                                                                                                                                                                                                                                                           .169
                                                                                                                                                                                                                                                                  label=
                                                                                                                                                                        Binding-site
                            19-JUL-2000
             AAY91885;
                                                                                       Mammalia.
                                                                                                                                                                                                                                                                                       Domain
                                                                                                      Key
Domain
                                                                                                                             Domain
                                                                                                                                            Domain
                                                                                                                                                          Domain
                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                Domain
```

```
Ushio S, Nukada Y,
                                                                                                                WPI; 2001-275206/29
                                                                                                                           N-PSDB; AAC85680
                                                                                                                                                                                                                                                                                                                   Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP2001231578-A.
                                             15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2001
18-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG68116;
                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG6811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                       The present sequence is an alternative primate interleukin-1 like molecule, designated IL-1-zeta. The 12 beta strands indicated in the features table, fold into a beta-trefoil fold. The specification claims an isolated or recombinant polypebtide that: (a) specifically binds colyclonal antibodies generated against at least a 12 consecutive amino acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see AAY91885); and (b) comprises at least one sequence selected from: AAY91886-903 or AAY91904-06. The preferred 12 consecutive amino acid segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to play a role in systemic inflammatory reactions, such as fever, hypoglycemia, reduced plasma iron and zinc, the acute response of the live, and increase plasma copper. IL-1-zeta binding compounds (comprising antigen binding sites) and IL-1-zeta polypeptides are also useful for both diagnostic and therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                         ů
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                        New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful for diagnostic and therapeutic purposes, comprises a 128 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;
natural killer activity; immune system; gene therapy; immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                               Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1165; DB 3; 100.0%; Pred. No. 1.9e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                      Claim 1; Page 103-104; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB47186 standard; protein; 218 AA
            99WO-US020868
                                   98US-00156966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL-1 related polypeptide.
                                                          (SCHE ) SCHERING CORP
                                                                                                       WPI; 2000-283588/24.
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                   N-PSDB; AAA08513
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1092773-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                   18-SEP-1998;
            17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    datches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB47186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                ведиепсе
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>6</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
YCDKDKCKGSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDKDKGQSHPSLQLKKBKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an interleukin-1 (IL-1)-related polypeptide. IL-1 related polypeptide was isolated from HPB-MLT cells, FERM-BP-2430, an established human T-cell line. IL-1 related polypeptide is useful for inhibiting natural killer (NK) activity, which is related to the immune system of mammals. The DNA encoding the IL-1 related polypeptide is useful in gene therapy of patients in need of NK activity inhibition and others suffering from immunodeficiency
                                                                                                                                                                                                                                                                                                                                                   New human interleukin-1-related polypeptide and polynucleotide, useful for gene therapy and in developing drugs as regulators of natural killer activity, are capable of inhibiting natural killer activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1165; DB 4; 100.0%; Pred. No. 1.9e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin 1 family protein SEQ ID NO:2.
                                                                                                                                                                                            Kurimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                               (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z
                                                                                                                                                                                            Yamamoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG68116 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 12; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2000; 2000JP-00372864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00349780.
11-OCT-2000; 2000EP-00308948
                                                               99JP-00294493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 218; Conservative
```

ö

```
The invention relates to an isolated or recombinant nucleic acid encoding interleukin-1zeta polypeptide. The invention is useful in gene therapy. The composition and methods are useful in diagnosing or treating degenerative or abnormal conditions which directly or indirectly involve development, differentiation or function, e.g. of the immune system and/or haematopoietic cells. The invention may also be used for preventing or treating other diseases or disorders associated with abnormal expression or triggering of response to the interleukin, such as inflammatory disorders, infection, allergies or cancer. The present sequence is human interleukin-1zeta variant.
                                                                                                                       New nucleic acid molecules encoding mammalian interleukin-1 polypeptides, useful for diagnosing, preventing or treating diseases associated with abnormal expression of interleukin, e.g. inflammation, infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSNNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; interleukin 1 zeta; IL-1 zeta; immmunogen; antisera production; antibody production; anti-inflammatory; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1165; DB 8;
100.0%; Pred. No. 1.9e-117;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin 1 zeta (IL-1zeta) segid 4.
                                                                                                                                                                                          Claim 2; SEQ ID NO 4; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL15868 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0100948P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2003; 2003US-00695195.
          98US-0100948P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                   (SCHE ) SCHERING CORP
                                                                                     WPI; 2004-189656/18.
N-PSDB; ADJ88305.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 218; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004068099-A1.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1998;
          18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-2004
                                                             Timans JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL15868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL15868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                              YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                  SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                 9
                                                                                                                             The present sequence represents a human interleukin 1 (IL-1) family protein having a combining affinity to a receptor of a protein of human IL-1 family higher than Tango-77. The protein is useful for the development of diagnostic, treating and/or preventive agents for various
                                                                                                                                                                                                                                                                                                        SIHDQDHKVLVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin-1zeta, gene therapy, immune system, haematopoietic cell; inflammatory disorder; infection; allergy, cancer; human.
                                                               family protein, used for the development of diagnostic and
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                      Length 218;
                                                                                                                                                                                                                                                                IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                    100.0%; Score 1165; DB 4; ilarity 100.0%; Pred. No. 1.9e-117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin-lzeta protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .50
..a= "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Epitope"
156. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Epitope"
                                                                                                        Claim 1; Page 30; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ88306 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00398412
  (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163. .169
/note= "Ep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ov. .41
/note= "F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
46..60
                          WPI; 2001-609968/70.
N-PSDB; AAI71179.
                                                                                                                                                                                                                                                    Similarity
                                                                                 treatment agents
                                                                                                                                                                                                               Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6680380-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-2004.
                                                                                                                                                                                                                                                       Best Local Simi
Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ88306;
                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                      diseases
                                                                   II-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ88306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         đ
                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                               ζ,
                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                               ò
```

ô

Gaps

ö

Indels

120

9

180

Ź

us-10-695-195-4.rag

```
Sequence 218 AA;
                                                                                             WO2004032837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
                                                                                                                                                                             08-OCT-2002;
                                                                                                                                                                                                        (ARES-) ARES
                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2004
                                                                                                                        22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO04679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                  diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
ADO04679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ***
유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                   The invention describes an isolated or recombinant interleukin 1 zeta polypeptide (I) that specifically binds to polyclonal antibodies consecutive amino acids segment of two fully defined sequences (S1) and (S2) having 218 amino acids as given in the specification and comprises at least one sequence chosen from (S1) and (S2) having 218 amino acids as given in the specification and comprises at least one sequence chosen from (S1) and (S2). Also described are: a fusion protein comprising (I) or its sequence or sequence of another cytokine or chemokine; a binding compound composition of matter comprising a sterile polypeptide (I) or (II) an antigen binding site from an antibody, which specifically binds to (II), (I) or (II) and a carrier such as an aqueous compound e.g., water, saline and/or buffer, where the carrier is formulated for oral, rectal, cand, (D) that encodes (I) or several antigenic peptides of (S1) or (S2); a cell (IV) transformed with (III); a method of modulating a cell (IV) transformed with (III); a method of modulating a conjust or antigonist of (I); a kit comprising a compartment of (I), (II) or (III) and/or instructions for use or disposal of reagents in the kit; complex. (I) is useful for developing more effective anti-inflammatory complex. (I) is useful for developing more effective anti-inflammatory contractions in the amino acid sequence of a human interleukin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine-1; interleukin-18BP; IL-18BP; cytokine-2; IL-1; IL-1F7b; IL-18R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                         ав
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNINPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                       Novel isolated or recombinant interleukin 1 zeta polypeptide useful a
immmunogen for producing specific antibodies or for developing anti-
inflammatory therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1165; DB 8; 100.0%; Pred. No. 1.9e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of human IL-1F7b.
                                                                                                                                                                             Claim 1; SEQ ID NO 4; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN41836 standard; protein; 218
99US-00398412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                WPI; 2004-304623/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                              N-PSDB; ADL15867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zeta polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 218 AA;
                         (TIMA/) TIMANS
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218;
                                                      Timans JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN41836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #X#X#X#X#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
The specification describes a method for using a cytokine-1 capable of binding to interleukin (IL)-188P and capable of inhibiting a receptor of a cytokine-2 that is a member of the IL-1 family, in the manufacture of a medicament for the treatment or prevention of a disease which is caused or aggravated by inducing the receptor of cytokine-2. The cytokine-1 is preferably IL-1FD. The receptor of cytokine-2. The cytokine-1 is useful for the treatment or prevention of inflammatory diseases, selected from endotoxin lethality (sepsis), liver injury induced by toxins or activated T cells or hepatitis C, arthritis, lung injury, psoriasis, inflammatory bowel diseases, brain injury, ischaemic injury, cardiac dysfunction, and neuritis, and for preventing metastesis formation. The present sequence represents human IL-1F7b, which is used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a cytokine-1, its isoform, mutein or fused protein, capable of binding to IL-18BP and inhibiting a receptor of a cytokine-2 that is a member of the IL-1 family, useful for treating or preventing inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
inflammatory disease; endotoxin lethality; sepsis; liver injury; hepatitis C; arthritis; lung injury; psoriasis; inflammatory bowel disease; brain injury; ischaemic injury; cardiac dysfunction; neuritis; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1165; DB 8;
100.0%; Pred. No. 1.9e-117;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 1; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO04679 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bufler
                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2003; 2003WO-US031378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0416827P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRADING SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dinarello CA, Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-340785/31.
```

ö

```
WO200036108-A2
                                          Homo sapiens.
                                                                                                         14-DEC-1999;
                                                                                                                               14-DEC-1998;
10-NOV-1999;
                                                                                     22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             음
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                       New isolated or recombinant interleukin-1 zeta polypeptide and related reagents such as antibodies, useful for treating inflammatory disease and as probes for diagnosing immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to interleukin-1 zeta polypeptide and polynucleotide. The agonist or antagonist of the interleukin-1 zeta is useful in modulating a cell that is involved in inflammatory response. The peptide fragments of IL-1 zeta are useful in research and diagnostic tools in the study of inflammatory reactions to antigenic challenge and the development of more effective anti-inflammatory therapeutics. Interleukin-1 zeta is useful in regulation and/or development of immune system. A polynucleotide encoding IL-1 zeta is useful for detecting the expression level of the polypeptide in a patient suspected of having an immunological disorder. The present sequence is a human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                       Interleukin-1 zeta variant; inflammatory reaction; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1165; DB 8; Length 218; 100.0%; Pred. No. 1.9e-117; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHCHELLER CATOKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNCNEPVGVTDKFENRKHIEFSFOPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interleukin-1 zeta splice variant TDZ.1.
                               IL-1 zeta; immunological disorder; human.
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
  Human interleukin-1 zeta variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY95299 standard; protein; 218
                                                                                                                                            98US-0100948P.
99US-00398412.
                                                                                                                        27-OCT-2003; 2003US-00694978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                          WPI; 2004-374758/35.
                                                                                                                                                                             (TIMA/) TIMANS J C.
                                                                                                                                                                                                                                    N-PSDB; ADO04678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 218 AA;
                                                                            US2004087766-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                        zeta variant
                                                                                                                                              18-SEP-1998;
                                                        Homo sapiens
                                                                                                                                                         17-SEP-1999;
                                                                                                  06-MAY-2004
                                                                                                                                                                                                    Timans JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY95299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY95299
ID AAY9
XX
AC AAY9
XX
DT 12-S
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
The present sequence is that of splice variant TDZ.1 (testis-derived zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is correspond most strongly in the kidney, skeletal muscle, testis, prostate, covary, colon, small intestine, liver, placenta, lung, tonsil, foetal liver, lymph node and bone marrow. The invention is directed to novel, purified and isolated IL-1 zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301), the nucleic acids (see AAX918-22) colon, such polypeptides, and their uses. The polypeptides can be used to study cellular processes such as immune regulation, cell proliferation, cell magnation, cell interaction and inflammatory cresponses, to identify proteins associated with IL-1 zeta, to screen for potential inhibitors, and to prepare antibodies. In particular, they can be used to activate and/or inhibit the induction of local cissue destruction and fever, inhibit the induction of local cissue destruction and fever, inhibit the induction of local cissue destruction and fever, inhibit the induction of inhibit the colls to screen for vascular endothelial cells to produce IL-6, induction of inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for identifying genes associated with diseases such as glaucoma, and insulindependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPTMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIHDODHKVIVIDSGNIJAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGFFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          induction of prostaglandins, nitric oxide synthetase, and metalloproteases, and upregulate and/or inhibit the upregulation of molecules on the surface of vascular endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.7%; Score 1161; DB 3; Length 218; 99.5%; Pred. No. 5.2e-117; ive 0; Mismatches 1; Indels (
Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.
testis-derived zeta variant; therapy; inflammation; fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 11; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Born TL;
                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0112163P.
99US-0164675P.
                                                                                                                                                                                                                                                                                                                                                99WO-US029549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442387/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sims JE, Smith DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA27920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 218 AA;
```

ö

120

```
31-OCT-2000
                                                                                   04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96940;
                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                       Domain
                                              Domain
        Domain
원
                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋩
                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                         Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis; psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer; anaemia; inflammatory boul disease; acute neuropathology; shock; chronic neuropathology; respiratory disease syndrome; restenosis; acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic; anti-arthritic; anti-psoriatic; antibacterial; immunosuppressive; anti-anaemic; neuroprotective; vasotropic; anti-human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              154. 160
|Tabel= Beta_strand
161. 1164
| hote= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70. .174 --
note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175. .179
/label= Beta_strand
180. .186
/note= "Variable loop region involved in receptor
                                                                                                                                                                                                            "Variable loop region involved in receptor
                                                                                                                                                                                                                                                  "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                      97. .107
/note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                             108. il3
|Tabel= Beta_strand
114. il17
|note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                 24. .131 -
note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Variable loop region involved in receptor
                                                                                                                                                                                        50. .64
/label= Beta_strand
55. .67
                                                                                                                                                                                                                                                                  77. .79
/label= Beta_strand
                                                                                                                                                                                                                                                                                                         10. .96
'label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                   18. .123
label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                          .32. .138
'label≈ Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65. .169
label= Beta_strand
                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                   label= Beta_strand
                              AAY70927 standard; protein; 218 AA.
                                                            (first entry)
                                                                                                                                                                                                                    binding"
                                                                                                                                                                                                                                           73. .76
/note= "
                                                                                                                                                                                                                                                           binding"
                                                                                                                                                                                                                                                                                                 binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         inding"
                                                                                                                                                                                                                                                                                                                                      binding"
                                                                                                                                                                                                                                                                                                                                                                            "binding
                                                                                                                                                                                                                                                                                                                                                                                                                  binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "inding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding"
                                                                                                                                                                                                                                                                                 80. .89
                                                                            Human zilla4 protein.
                                                                                                                                                                sapiens
                                                            05-SEP-2000
                                                                                                                                                                               Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                HOMO
```

```
The present sequence is the human interleukin (IL)-1 homolog zillad protein. This protein contains a core structure of 12 beta-strands wound into a beta-barrath, with the beta-strands seperated from each other by loops. The loops between these beta-strands are highly variable among the family members and are believed to be involved in receptor binding. The sallad proteins modulate inflammation and other immunological processes and are therefore useful for treatment of arthritis, psoriasis, septic shock, graft-versus-host disease and leukaemia. Other diseases that may be modulated by zillad proteins include cancer, aneamia, inflammatory bowel disease, acute and chronic neuropathologies, shock, respiratory disease syndrome, restenosis and acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIHDQDHKVLVIDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
disease, leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                   187. .189
//label= Beta_strand
190. .200
/note= "Variable loop region involved in receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1154; DB 3; Length 218;
Pred. No. 3e-116;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                        201. .204
/label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96940 standard; protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 2; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00179614.
                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US025038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.1%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao
                                                                                                                                                               binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC
binding'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             West RR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350740/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD00210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 218 AA;
                                                                                                                                                                                                                                                                                        WO200024899-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1999;
```

ö

(first entry)

standard; protein; 218 AA.

(first entry)

```
13-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                  AAB28266;
                                               AAB28266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                RESULT 11
                                  AAB28266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      움 🌣
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated nucleic acid molecule encoding an interleukin-1-like polypeptide (IL-11p) that retains one or more activities of the peptide from which it is derived, such as the IL-18R binding activity of a human interleukin-1 receptor antagonist-1 (hIL-18A) polypeptide, is new. The nucleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for recombinantly producing the IL-11p polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and cheeses (conversels) gene therapy protocols may be used to supplement a patients production of the polypeptide or to rectify mutations that lead to the production of in active peptides). The peptides produced may be used to supplement apply protein expression and activity which may be use to treat disorders associated with inappropriete IL-11p expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g.
use to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity, such as inflammatory disorders, asthma, arthritis, osteoarthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                               hIL-1RalV; human interleukin-1 receptor antagonist-1; IL-11p; osteopathic; interleukin-1-1ike polypeptide; anti-inflammatory; anti-asthmatic; anti-arthritic; antimicrobial; respiratory; accine; anti-ischemic; dermatalogical; immunomodulatory; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding interleukin-1-like polypeptides, useful for preventing and treating e.g. inflammation, asthma and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1154; DB 3; Length 218; Pred. No. 3e-116; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CNCNEPVGVTDKPENRKHIEFSFQPVCKAEMSPSEVSD 218
Human IL-1 receptor antagonist 1 V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Fig 19; 143pp; English.
                                                                                                                                                                                                                                                                                98US-0113430P.
99US-0116843P.
99US-0129122P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%;
99.1%;
                                                                                                                                                                                                                                               99WO-US030720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452395/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 216; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Pan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 218 AA;
                                                                                                                                                                            WO200039297-A2.
                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                 22-DEC-1999;
                                                                                                        gene therapy
                                                                                                                                                                                                                                                                                   23-DEC-1998;
                                                                                                                                                                                                                                                                                                      22-JAN-1999;
13-APR-1999;
                                                                                                                                                                                                               06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                            Soddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
```

%XCCCCCCCCCCCCCCCCCX

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        įв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-1 homolog useful for treating conditions such as chronic and acute inflammation, septicemia, autoimmune diseases ischemia, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 useful for treating conditions such as chronic and acute inflammation, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis, and arthritis), transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease, allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g. osteoporosis), cancer, congestive heart failure, atherosclarosis, and Alzheimer's disease, trelated to either an excess of, or an underexpression of, IL-1H4 polypeptide activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPF1FYRAQVGSWNMLBSAAHPGWF1CTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSFYGENSGVKWGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; interleukin-1 homologue; IL-1H4; inflammation; septicaemia; autoimmune disease; inflammatory bowel disease; psoriasis; arthritis; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease; allergy; asthma; restenosis; brain injury; AIDS; bone disease; osteoporosis; cancer; congestive heart failure; atherosclerosis; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%; Score 1154; DB 3; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory disease, allergies, and asthma
homologue IL-1H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 28-29; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00293625.
                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-2000; 2000WO-US010207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young PR, Mcdonnell PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-687155/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC66727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 218 AA;
                                                                                                                                                                                                                                                                                                             WO200063226-A1.
                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                     26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
```

ö

셤 δ 셤 ઠે 셤 ઠે

ò

```
SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCDKDKGGSHPSLQLKKEKLMKLAAQKESARPFIFYRAQVGSWNMLESAAHPGWFICTS 180
YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%; Score 1154; DB 8; Length 218; 99.1%; Pred. No. 3e-116; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                    CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                  antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schoenfeld J,
                                                                             CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; SEQ ID NO 1406; 3069pp; English.
                                                                                                                                                                                                                                                                                                                                           Antipsoriatic protein sequence #686
                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jackman J,
                                                                                                                                                                                                                    ADN05012 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2003; 2003WO-US030907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2002; 2002US-0414006P.
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-305105/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADN05011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                   01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Simi
Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bodary S,
                                     121
                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
  121
                                                                             181
                                                                                                                                                                                                                                                              ADN05012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ę,
                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                               셤
                                                                             ò
                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypoptide. The IL-114 polypoptide can be expressed by steadard recombinant methodology. The IL-114 polypoptide polymucleotides and modulators are useful for treating chronic and acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory bowel disease, disease, infection, stroke, ischemia, acute respiratory disease syndrome, allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g., osteoporosis), cancer (e.g., lymphoproliferative disease (e.g., osteoporosis), cancer (e.g., lymphoproliferative disease (e.g., polymucleotides are useful as diagnostic reagents and for chomosome identification. The present sequence represents the IL-114 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSFVGENSGVKMGSEDWEKDEPOCCLEDPAGSPLEPGPSLPTMNFVHTSPKVKNLNPKKF 60

    .218
    /note= "specifically claimed mature protein (AAB85138)"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                               Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic; immunosuppressive; antipsoriatic; antiathritic; oyfostatic; antilaIV; cerebroprotective; antiathratic; vasotropic; vulnerary; osteopathic; immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute inflammation, septicemia, autoimmune diseases, transplant rejection, graft versus host disease, stroke, ischemia, allergy and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides an isolated interleukin-1 homologue, IL-1H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1154; DB 4; Length 218;
Pred. No. 3e-116;
0; Mismatches 2; Indels (
                                                                                                                                                          Interleukin-1 homologue (IL-1H4) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                     1. .20
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                         Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 29; 30pp; English.
                                         AAB85136 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-2000; 2000WO-US032521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00452140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Д,
                                                                                                                                                                                                                                                                                   therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-389949/41.
N-PSDB; AAF84120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcdonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200140247-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1999;
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                      22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-2001
                                                                               AAB85136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kumar S,
                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                   gene
  RESULT 12
```

ö

셤 ð

σ

```
The present sequence is a variant of human interleukin (IL)-1 homolog zilla4 protein, consisting of Asp in place of Glu at position 200. The replacement of Glu (200) with Asp results in attenuation of protein inflammation and other immunological processes and are therefore useful for treatment of arthritis, psoriasis, septic shock, graft-versus-host disease and leukaemia. Other diseases that may be modulated by zilla4 proteins include cancer, ansemia, inflammatory bowel disease, acute and chronic neuropathologies, shock, respiratory disease syndrome, restenosis and acquired immune deficiency syndrome. Note: The present sequence is not shown in the specification but is derived from human zilla4 protein sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YCDKDKGGSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWMLESAAHPGWFICTS 180
                                                                                                                                                   Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis; psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer; anamemia; inflammatory bowel disease; acute neuropathology; shock; chronic neuropathology; respiratory disease syndrome; restenosis; acquired immune deficiency syndrome; ALDS; antiinflammatory; cytostatic; anti-approfici, antibacterial; immunosuppressive; anti-anaemic; neuroprotective; vasotropic; variant; anti-human immunodeficiency virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ၀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
disease, leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1151; DB 3;
Pred. No. 6.3e-116;
1; Mismatches 2;
                               Ş
                                                                                                                          Human zilla4-E200D variant protein.
                              AAY71084 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00179614
                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US025038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 98.5
Matches 215; Conservative
                                                                                            (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350740/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                       WO200024899-A2
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-1998;
                                                                                          05-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                              AAY71084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       West RR,
RESULT 14
                  AAY71084
                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
New interleukin-1 homolog Zilla4 protein, useful for modulating an immune response and for treating diseases, e.g., inflammatory diseases, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; interleukin-1 homologue; IL-1; zilla4; immune response;
inflammatory disease; cancer; anaemia; immunomodulator; antiinflammatory;
cytostatic; antianaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of human interleukin-1 (II) homologues designated zilla4, and the polynucleotide sequences that encode them. The gene encoding human zilla4 is located on chromosome 2. Also disclosed is a method of making these proteins and a method of modulating an immune response. The proteins are useful for treating diseases such as inflammatory diseases, cancer, and anaemia. The present sequence represents human zilla4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.0%; Score 1151; DB 7; Length 218; 98.6%; Pred. No. 6.3e-116; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
            CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 2; 44pp; English.
                                                                                           Ė
                                                                                           ADH89067 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                  22-NOV-2002; 2002US-00302554.
                                                                                                                                                                                                                                                                                                                                                           98US-0105824P.
99US-00428118.
                                                                                                                                                                                                                                                                                                                                                                                                                              gao
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                       Human zilla4 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                            West RR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-897576/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADH89066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 218 AA;
                                                                                                                                                                                                                                                                               US2003148467-A1.
                                                                                                                                                                                                                                                                                                                                                           27-OCT-1998;
27-OCT-1999;
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                            22-APR-2004
                                                                                                                                                                                                                                                                                                          07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anemia.
                                                                                                                     ADH89067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
 181
                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                  15
                                                                                ADH89067
                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                    셤
  ઠે
```

ö

9 9

II)

180

Search completed: September 29, 2005, 11:12:56 Job time : 65.5 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model OM protein - protein search, September 29, 2005, 11:04:58; Search time 25.5 Seconds (without alignments) 822.559 Million cell updates/sec Run on:

US-10-695-195-4 1165 1 MSFVGENSGVKMGSEDWEKD.....IEFSFQPVCKAEMSPSEVSD 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	interleukin-1 rece	interleukin-1 rece			interleukin-1 rece		_	 	_	_	interleukin-1 beta	-	interleukin-1 beta	•	interleukin-1 beta	interleukin-1 alph	glucan 1,3-beta-gl	hypothetical prote	chitin synthase (E	hypothetical prote	imbibition protein	probable membrane	DNA topoisomerase	transcription fact	conserved hypothet	hypothetical prote	hemolysin UU436 [i	a)	hypothetical prote
	ID	JC7104	A44610	A54377	A30368	A39386	C40956	823010	S38373	JN0724	ICB01B	I55969	ICH01B	JC5646	S34031	A30584	ICMS1	JN0118	T17291	T18220	S54460	T46188	867053	T04488	S15342	F71369	T04426	C82891	I56329	T24522
	DB	8	•	•	•	7	•	7	7	-	<del></del>	-	-	8	7	-				~									7	7
	Query Match Length DB	155	178	177	177	180	178	566	267	267	566	269	269	214	404	268	270	448	845	1026	471	773	776	1179	557	740	1405	247	425	425
de	Query Match	14.8	13.6	12.9	12.8	12.8	12.4	10.9	10.5	10.3	9.7	9.1	0.	8.5	7.8	7.6	7.3	7.1	7.1	7.1	7.0	7.0	7.0	6.9	6.8	8.9	6.8	6.7	6.7	6.7
	Score	172.5	159	150.5	149.5	149.5	144.5	127.5	122	119.5	112.5	106.5	104.5	95	91	68	85	83	82.5	82.5	82	81	81	80	79.5	79.5	79	78.5	78	78
	Result No.	-	8	m	4	Ŋ	φ	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

triacylglycerol li ABC transporter-li	probable ubiquitin hypoxia-inducible	probable ctpH prot	zinc iinger protei	Dicact Ovarian can	procein-giudamace	triacyigiycero, ii	triacylglycerol li	protein-glutamine	protein F9C16.25	hypothetical prote	AF-9 protein - hum	_	dynein light chain
S41095 T46101	F84601	G70630	I84499	ASSBAL	F70151	S41096	PN0493	A45321	D96504	C87358	139411	D86164	T02846
0 0	90	1 00	ο,	-	~	N	н	N	~	7	7	7	7
544	700	1539	1706	1863	375	544	563	764	772	859	268	571	627
6.7	6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9
78	77.5	77.5	77.5	77.5	77	77	77	77	77	77	76.5	76.5	76.5
30	35	34	35	36	37	38	39	40	41	42	43	4	45

## ALIGNMENTS

RESULT JC7104 interle C, Speci	RESULT 1 JC7104 C.Species: Homo sapiens (man) C.Species: O3-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Acce R;Mule	C;Accession: UC'1104 Kymilero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, Biochem Biochive Ree, Commun. 263, 702-706, 1999
A;Titl	A.Title: ILIHTI: A novel interleukin-1 receptor antagonist gene. A;Reference number: JC7104; MUID:99443727; PMID:10512743
A;Acce A;Mole	A;Accession: JC7104 A;Molecule type: mRNA
A;Resi A:Cros	A;Residues: 1-155 <mul> A:Cross-references: UNIPROT:Q9UBH0; GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g60</mul>
C, Genetics:	tics:
A; Gene A; Map C; Keyw	Yapene: 11.11.y1 A.jkap position: 2q14 C;Keywords: macrophage
Onez	Query Match 14.8%; Score 172.5; DB 2; Length 155;
Best	Best Local Similarity 33.6%; Fred. No. 7.35-09; Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
ò	60 FSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKG 106
q	:           :
ò	107SPILLGUSKGEFCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS 163
g	53 SLSPVILGVQGGSQCLSCGVGQ-EPTLTLEPVNIMELYLGAKESKSFTFYRDMGL 107
ò	164 WIMLESAAHGWFICTSCNCNEPVGVTDKFEN 195
q	108 TSSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139

interleukin-1 receptor antagonist precursor - mouse
N;Alternate names: IL-IRa
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A44610; B40956; A49031; IS6106; IS2970
R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
R;Matsushime, H.; Roussel, M.F.; Matsushima, R.; Hishinuma, A.; Sherr, C.J.
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph A;Reference number: A44610, MUID:91316273; PMID:1830498
A;Accession: A44610
A;Accession: A44610
A;Residues: 1-178 «MAT>
A;Residues: 1-178 «MAT>
A;Cross-references: UNIPROT:P25085; GB:M64404; NID:919826; PIDN:AAA39277.1; PID:91982:R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson

```
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A40956
A;Molecule type: DNA
A;Residues: 1-177 <BIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S08160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: I37894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 23-178 45HU2
A; Residues: 23-178 45HU2
A; Cross-references: GB: S64082; NID: 9238584; PIDN: AAB20265.1; PID: 9238585
A; Cross-references: GB: S64082; NID: 9238585
A; Experimental source: perincal macrophages, ICR strain
A; Note: sequence extracted from NCBI backbone (NCBIN: 64082, NCBIP: 64085)
B; Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
A; Immunol. 146, 4228-4233, 1991
A; Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mappin
A; Reference number: I56106; MUID: 91250712; PMID: 1828262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin-1 receptor antagonist secreted form precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54377; 146729
R;Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 662-6971, 1994
A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara A;Reference number: A54377; MUID:94165101; PMID:7509813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA

A Residues: 1-178 < RES.

A; Residues: 1-178 < RES.

A; Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388

R; Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.

Cytokine 6, 1-9, 1994

A; Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat

A; Reference number: I52970; MUID:94271931; PMID:8003626
Froc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family;
A;Reference number: A40956; MUD:91271363; PMID:1828896
A;Accesion: B40956
A;Molecular Companiar C
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A;Title: Cloning, heterologous expression and characterization of murine interleukin 1
A;Reference number: A49031; MUID:92037824; PMID:1834470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 FSIHDQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSSASAEKGSPILLGVSKGEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 CLSCAKSGDDI--KLQLEEVNITDLSKNKEEDKR-FTFIRSEKGPTTSFESAACPGWFLC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 CLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFIC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: IL-1rn
A;Introns: 40/2; 70/1; 107/3
C;Superfamily: interleukin-1
C;Keywords: cytckine receptor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;1-76/Product: interleukin-1 receptor antagonist #status predicted <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 FRIWDTNQKTFYLRNNQLIA----GYLQGPNI--KLEEKIDMVPIDLHS-VFLGIHGGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:L32838; NID:9487864; PIDN:AAA20576.1; PID:9528978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.6%; Score 159; DB 2; Length 178; 32.7%; Pred. No. 1.6e-07; Ative 23; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 TSCNCNEPVGVTDKFENRKHI-EFSFQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 32.7%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                              A, Molecule type: DNA
A, Regidues: 7-178 <EIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: A54377
A, Molecule type: mRNA
A, Residues: 1-177 <COM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: I56106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: 152970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
A;Cross-references: UNIPROT:P26890; GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g54574
A;Experimental source: colon tissue
A;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
A;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
Immunology 77, 235-244, 1992
A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text change 09-Jul-2004
C;Accession: A40956; I37894; A30368; S08160; S08159; A37822
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson Proc. Natl. Acad. Sci. U.S.A. 88, 5222-5236, 1991
A;Title: Interleukin i receptor antagonist is a member of the interleukin 1 gene family A;Reference number: A40956; MUID:91271363; PMID:1828896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P18510; GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186388; R;Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, i Cytokine 4, 83-89, 1992.
A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist A;Reference number: 137894; MUID:92338323; PMID:1385987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; T Asture 344, 633-638, 1990
A;Title: Purification, cloning, expression and biological characterization of an interl A;Reference number: A30368; MUID:90220867; PMID:2139180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-177 < CAR>
A; Residues: 1-177 < CAR>
A; Residues: 1-177 < CAR>
A; Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
A; Cross-references: GB:X53296; NID:g12578; PIDN:CAA37386.1; PID:g32579
A; Note: parts of this sequence, including the amino end of the mature protein, were con-R; Risenberg, S.P.; Brans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; Nature 343, 341-346, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Primary structure and functional expression from complementary DNA of a human A;Reference number: S08160; MUID:90136921; PMID:2137201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VPDKNYIRPEIFFALASSLSSASA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 EKGSPILLGVSKGEFCLYCDK--DKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LGIQRGKLCLSCVKSGDKMKLH----LEAVNITDLGKNKEQDKR-FTFIRSNS 130
                                                                                                                                                                                                                                                                                                                                                                 A;Accession: 146729
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Accessitus: 1-177 <GGT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukfin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 FRIWDVNOKTFYLRNNQLVAGYLQGPNAKLEERIDVVP----LEPQLLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.9%; Score 150.5; DB 2; Length 177; Best Local Similarity 28.0%; Pred. No. 1e-06; Matches 42; Conservative 21; Mismatches 42; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-1 receptor antagonist secreted form precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 GSWNWLESAAHPGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <LEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 FSIHDQDHKVLVLDSGNLIA-
```

ģ

11;

```
A,Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor
C;Keywords: alternative splicing; cytokine receptor
F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #sta
F;1-180/Product: interleukin-1 receptor antagonist, short intracellular splice for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interial proceptor antagonist precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Accession: C40956
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family A;Accession: C40956
A;Accession: C40956
A;Accession: C40956
A;Accession: C40956
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-178 <EIS>
A;Cross-references: UNIPROT:P25086; GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g20492
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 FSIHDQDHKVLVLDGGNLIA------VPDKNYIRPEIFFALASSLSSASAEKGSPIL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNWLESA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 LGIHGGKLCLSCVKSGDDT--KLQLEEVNITDLNKNKEEDKR-FTFIRSETGPTTSFEL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (domestic sheep)
#text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                            39 FRIWDTNQKTFYLRNNQLIAGYLQGPNTKLEBKIDMVPIDF-------RNVF
                                                                                                                                                                                                                                                                                                                                                                           53 KNINPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSSASAEKGSPILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-1 beta precursor - sheep
NyAlternate names: hematopoietin-1; IL-1 beta
NyAlternate names: hematopoietin-1; IL-1 beta
NyAlternate names: hematopoietin-1; IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S23010; S43047; S13092; B61246
SysSeow, H.F.; Rochel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A,Title: Nucleotide sequence of ovine macrophage interleukin-1 beta CDNA.
A,Reference number: S23010; MUID:92119335; PMID:1840515
A,Accession: S23010
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; Score 144.5; DB 2 29.1%; Pred. No. 3.8e-06; iive 20; Mismatches 53
                                                                                                                                                                                                                                             12.8%; Score 149.5; DB 2
29.3%; Pred. No. 1.3e-06;
tive 28; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ACPGWFLCTTLEADHPVSLTN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 AHPGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-1 receptor antagonist, long intracellular splice form - human N; Contains: interleukin-1 receptor antagonist, short intracellular splice form N; Contains: interleukin-1 receptor antagonist, short intracellular splice form C; Speciess: Home sapies (man) C; Speciess: Home sapies (man) C; Speciess: Home sapies (man) C; Spacession: 137893; A3936 C; Rybuzio, M.; Pollartarutti, N.; Sironi, M.; Polli, G.; De Gioia, L.; Introna, M.; Mantovan J; Ryp. Med. 182, 623-628, 1995
A, Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant A, Accession: 137893
A, Accession: 137893
A, Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT: P18510; EMBL:X84348; NID:91008970; PIDN:CAA59087.1; PID:9100 R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.; Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685; 1991 A;Title: CDNA cloning of an intracellular form of the human interleukin 1 receptor antag A;Reference number: A39386; MUID:91219436; PMID:1827201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: interleukin-1
;Reywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
;1-25/Domain: signal sequence #status predicted <SIG>
;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
                                                                                   P.L.; Ar
                                                                                                                                                                                                                                                 A; Molecule type: protein
A;Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R;Bienkowski, M.J.; Ressalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
J. Biol. Chem. 265; 14505-14511, 1990
A;Title: Purification and characterization of interleukin 1 receptor level antagonist px
A;Reference number: A37822; MUID:90354444; PMID:2143761
A; Residues: 1.7.7 cEI2>
A; Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
A; Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
B; Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; A Nature 343, 336-340, 1990
A; Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor. A; Reference number: $08159; MUID:90136920; PMID:2137200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSSASAEKGSPILL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Rebidues: 1-3.55-180 «HAS>
A;Cross-references: GB:MS5646; NID:G186291; PIDN:AAA59138.1; PID:g186292
C;Comment: For an alternative splice form, see PIR:A30368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: alternative splicing; cytokine receptor; extracellual profile 125/Domain: signal sequence #status predicted <SIG> P;1-25/Domain: signal sequence #status predicted <SIG> P;26-177/Product: interleukin-1 receptor antagonist #status experimental P;109/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 26-52,70-77;122-127;170-175 <BIE>
A;Esperimental source: culture medium, PMA-stimulated THP-1 cells
C;Comment: For an alternative splice form, see PIR:A39386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 12.8%; Score 149.5; DB 2
1 Similarity 29.3%; Pred. No. 1.3e-06;
41; Conservative 28; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
A;Introns: 39/2; 69/1; 106/3
C;Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 CPGWFLCTAMEADQPVSLTN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 HPGWFICTSCNCNEPVGVTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-180 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A37822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB:IL1RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

27;

Length 178; Indels

```
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-1 beta precursor - bovine
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 LYPNWYISTSQAEQKPV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 AHPGWFICTSCNCNEPV 187
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 QKPV 246
                                                                                                                                                                                                                                                                                                                                                                                                  184 NEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JL0010
50;
                                                                                                                                                                                                                                                                                  124
Matches
                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                       g
                                                                                                                                                                        ઠે
                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-144,'L',146-266 <AND>
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde Eur. J. Blochem. 217, 45-52, 1993
Eur. J. Blochem. 217, 45-52, 1993
A,Fitle: Gene sequence, cDNA construction, expression in Escherichia coli and geneticall A;Reference number: S38373; MUID:94039070; PMID:8223584
A,Accession: S39373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q29082; EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g4079
           A,Cross-references: UNIPROT:P21621; EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A,Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an additional to the EMBL Data Library, May 1992
A,Reference number: S43047
A,Accession: S43047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <FIS>
A; Crose: references: EMBL:X54796
A; Note: the authors translated the codon AGT for residue 62 as Arg
R; Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Imunology 74, 45-460, 1991
A; Title: Molecular cloning and characterization of ovine IL-lalpha and IL-lbeta.
A; Reference number: A61246; MUID:92120716; PMID:1769692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 KFSIHDQDHKVLVLDSG---NLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 KCKLQDREQKSLVLDSPCVLKALHLPSQEMSR-EVVFCM-SFVQGEERDNKIPVALGIRD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 GEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'L', 146-266 <SAR>
A; Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'L', 146-266 <SAR>
A; Cross references: BBBL:X54796; NID:91273; PIDN:CAA38566.1; PID:91274
B; Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A; Title: Nucleotide sequence of ovine interleukin-1 beta.
A; Reference number: S13092; MUID:91088326; PMID:2263490
A; Accession: S13092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 122; DB 2; Length 267; Pred. No. 0.00082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 beta precursor - pig
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change
C.Accession: 838373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%; Score 127.5; DB 1.
29.5%; Pred. No. 0.00025;
vative 26; Mismatches 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Introns: 16/2; 33/3; 99/1; 154/1; 197/3; Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.59
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| || : ||
234 YISTSQIEEKPV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 FICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-267 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: B61246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ৡ
```

```
C;Accession: JN0724
R;Huether, M.J; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
R;Huether, M.J; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
A;Hitle: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 by A;Reference number: JN0724; MUID:93314975; PMID:8325511
A;Accession: JN0724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: mRNA
A; Residues: 1-267 - AHDS.
A; Residues: 1-267 - AHDS.
A; Residues: 1-267 - AHDS.
A; Cross-references: UNIPROT: P26889; GB: M86725; NID: g164607; PIDN: AAA02584.1; PID: g164601
A; Experimental source: alveolar macrophage
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleava; C; Comment: This protein lacks a conventional signal sequence for protein export. Cleava; ved form of interleukin-lbeta, unlike interleukin 1-Alpha, is inactive.
C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-1: C; Superfamily: interleukin-1
C; Superfamily: interleukin-1
C; Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage; P; 115-267/Product: interleukin-1 beta #status predicted <111.5
F; 77/Binding site: myristate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: hematopoietin-1; IL-1 beta
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: JL0010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S. A;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S. A;Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin A;Reference number: A94695; MUID:88318652; PMID:3261832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 NINPKKFSIHDQDHKVLVLDSGNLIAVPD--KNYIRPEIFFALASSLSSASAEKGSPILL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVSKGEFCLYC-DKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESA 170
                                                                                                                                                                                                                                                             67 HKVLVLDSGNLIAVPD--KNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCLYC-D 123
                                                                                                                                                                                                                                                                                                                                                                                                                                    KDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTSCNC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
                                                                                 19 KDEPQ-----CCLEDPA---VSPLEPGPSL---PAMNFVHTSPKVKNLNPKKFSIHDQD
    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ئ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.0%; Pred. No. 0.0014;
Matches 37; Conservative 27; Mismatches 64; Indels 9
    77;
```

```
A;Status: translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                              94 SFIFEEEPILCDS--WDDDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: I51852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 118-269 <DAU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; II-1 beta
C;Species: War ausculus (house mouse)
C;Species: Je-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: I55969; A24719; S13029
R;Gray, P.W.; Glaister, D.; Chen, B.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the CDNA for mu A;Reference number: I55969; MUID:87058957; PMID:3491144
A;Accession: I55969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-26 cwal.
A;Cross-references: 1-26 cwal.
A;Cross-references: WINTROT: P09428; GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A;Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A;Reference number: S01380; MUID:89016591; PMID:3262866
A;Accession: S01380
                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-251, A', 253-266 <LEO>
A; Cross-reneces: EMBL:X12498; NID:9448; PIDN:CAA31018.1; PID:9449
A; Cross-reneces: EMBL:X12498; NID:9448; PIDN:CAA31018.1; PID:9449
C; Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
C; Comment: This protein-lacks a conventional signal sequence for protein cyport. Cleavag
C; Comment: Interleukin-lacks unlike interleukin 1-alpha, is inactive.
C; Superfamily: interleukin-lacks a precursor is less heavily myristoylated than interleukin-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNÅ
A; Residues: 1-260 <RES.
A; Residues: 1-260 <RES.
A; Cross-references: UNIPROT: P10749; GB: MIS131; NID: G198293; PIDN: AAA39276.1; PID: G309398
R; Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, B.; Melli, M.
R; Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
R; Telford, J.L.; Macchia, I. Apsta Gane: structure and evolution.
A; Reference number: A24719; MUID: 87117546; PMID: 3492706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA

A, Molecule type: mRNA

A, Cross-references: 1-269 < TEL>

A, Cross-references: GBX.04964; NID:952666; PIDN:CAA28637.1; PID:952667

A, Cross-references: GBX.04964; NID:952666; PIDN:CAA28637.1; PID:952667

R, Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I.

R, Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I.

A, Title: Reduction of biological activity of murine recombinant interleukin-lbeta by sell A, Reference number: S13029; MUID:91130610; PMID:1993481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFSIHDQDHKVLVLDSGNLIAVPD--KNYIRPEIFFALASSLSSASAEKGSPILLGVSKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 EFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.7%; Score 112.5; DB 3
Best Local Similarity 27.5%; Pred. No. 0.0064;
Matches 36; Conservative 25; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 ICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 ISTSQIEERPV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A24719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S13029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: IL-1-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   디
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à<u>.</u> 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
interleukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Peb-1986 #sequence revision 15-May-1998 #text change 09-Jul-2004
C;Accession: A25542; A29019; Ā94023; A93361; I51852; I65200; I38132; B27616; A01848; S1
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rc
A;Reference number: A25542; MUID:87040762; PMID:3490654
A;Accession: A25542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-5, K', 7-269 < CLA>
A; Charle the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu A; Noce: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu A; Noce: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu A; Reference number: A2019; MUID: 87248099; PMID: 2954882
A; Reference number: A2019; MUID: 87248099; PMID: 2954882
A; Residues: 1-269 < CENA
A; Reference number: A94023; MUID: 8088517; PMID: 6083565
A; Rocession: A94023
A; MOID: 8088517; PMID: 6083565
A; Residues: 1-5, K', 7-269 < CHARA
A; Residues: 1-5, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were confir-
R;Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: I51852
                                                             macrophage; mitogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 IHDQDHKVLVL-DSGNLIAVP-DKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------YR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 LYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICT
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine;
F;118-269/Product: interleukin-1 beta #status experimental <IL1>
                                                                                                                                                                                                                         DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                         Query Match 9.1%; Score 106.5; DB 1; Best Local Similarity 23.7%; Pred. No. 0.024; Matches 49; Conservative 37; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCNCNEPVGVTDKFENRKHIEFSFQPV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 SQAEHKPVFLGNN-SGQDIIDFTMESV 267
```

```
Query Match
Best Local Similarity
                                                                                                                                        Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1-214 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JC5646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S46077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Modecule type: protein
A; Residues: 117-13, X', 125-126, 'X', 128 < 25E>
A; Residues: 117-13, X', 125-126, 'X', 128 < 25E>
A; Residues: 117-13, X', 125-126, 'X', 128 < 25E>
R; Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Lockaley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A; Title: The 31-kba precursor of interleukin lalpha is myristoylated on specific lysines
A; Contents: annotation; myristylation of lysines
A; Contents: annotation; myristylation of lysines
A; Title: The role of arginine residues in interleukin lreceptor binding.
A; Title: The role of arginine residues in interleukin lreceptor binding.
A; Title: The role of arginine residues in interleukin lreceptor binding.
A; Tottle: The role of arginine residues in interleukin lreceptor binding.
A; Tottle: Modification of Arg-120 by phenylglyoxal blocks receptor binding
A; Contents: annotation; topformation by thenylglyoxal blocks receptor binding
A; Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
A; Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
A; Title: High-resolution three-diamensional structure of interleukin lbeta in solution by A; Title: High-resolution three-diamensional structure of interleukin lbeta in solution A; A; Title: High-resolution; Three-diamensional structure of interleukin lbeta in solution A; A; Title: Structure-function mapping of interleukin l precursors. Cleavage leads to a con A; Reference number: A39774; MUID:91201363; PMID:2016316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOKI. Akad. Nauk SSSR 309, 1005-1008, 1989
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin
A;Reference number: 138131; MUID:90249285; PMID:2635664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R;Zsebo, K.M.; Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K. Blood 71, 962-968, 1988
A)Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic A;Reference number: A90732; MUID:88184226; PMID:3281727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This protain lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;117-269/Product: interleukin-1 beta #status experimental <IL1>
                                                                                                  S.; Hira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspahr,
J. Mol. Biol. 209, 779-791, 198
A;Title: Crystal structure of recombinant human interleukin-lbeta at 2.0 angstrom resolu
A;Reference number: A44666; MUID:90064532; PMID:2585509
                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, ii, S.A.; Vinetskii, Y.P.
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: CDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line. A;Reference number: I52217; MUID:87156769; PMID:3493774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Contents: annotation
R,Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
aubmitted to the Brookhaven Protein Data Bank, December 1989
A, Reference number: A50016; PDB:111B
                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GDB:120094; OMIM:147720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2q13-2q21
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C;Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: 138132
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                       1-269 <NIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-269 < KOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: B27616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Gene: GDB: IL1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
```

```
C;Accession: JC5646
R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa, A;Til-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-1 A;Reference number: JC5646; MUID:97080493; PMID:8921838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:028386; DDBJ:D42165; NID:92463549; PIDN:BAA22528.1; PID:924. C;Comment: This protein mediates a variety of physiological response to infections and synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce C;Superfamily: interleukin-1
                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 AMNEVHTSPKVKNIN-PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSS 100
                                                                                                                                                                                                                                             45 FVHTSPKVKNLNPKKFSIHDQDHKVLVLDSG--NLIAVPDKNY-IRPEIFFALASSLSSA 101
                                                                                                                                                                                                                                                                                         102 SAEKGSPILLGVSKGEFCLYC--DKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                               168 SNDK-IPVALGLKEKNLYLSCVLKDDK----PTLQL--ESVDPKNYPKKKMEKRFVFNKI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AMSIIVAVEKLKKIPVPCSQAFQDDDLRSLF-----SVIFEEVVFCMSFVQGE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 BETDK-IPVALGLKEKNLYLSCGMKDGK--PTLQL--ETVDPNTYPKRKMEKRFVFNKME 166
F;76/Binding site: myristate (Lys) (covalent) (partial) #status experimental 
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Saccharomyces cerevisiae
Cibate: 30-Sep-1993 #text_change 09-Jul-2004
Cibate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
Cibacesion: S34031; S46077; S34928
RiJacquet, M.
Submitted to the EMBL Data Library, January 1993
A;Reference number: S34022
A;Reference number: S34021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Reaidues: 1-404 cJAC-
A;Cross-treferences: UNIPROT:P38130; EMBL:Z21487; NID:g311665; PID:g311682
R;Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                      Length 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%; Score 95; DB 2; Length 214; 24.5%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                      DB 1;
                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTR3 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBR1445; protein YBR205w
                                                                                                                                       Pred. No. 0.036;
                                                                                                                                   1. Similarity 29.1%; Pred. No. 0.03 43; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Mismatches
                                                                                                      Score 104.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 OVGSWNMLESAAHPGWFICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 VGSWNMLESAAHPGWFICTSCNCNEPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 EINNKLEFESAQFPNWYISTSQAENMPV
                                                                                                      9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: 846054
```

```
Search co
Job time
                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                         셤
                                                                                                      ઠે
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fac C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Accession: A27714; A30584; JU0082; A32166
R; Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M. Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A; Title: Cloning and sequence analysis of a CDNA for lymphocyte proliferation potentiating A; Reference number: A27714; MUID:88134238; PMID:2449207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:P14628
R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, G
L, Tmmunol. 142, 2299-2306, 1398
A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A;Reference number: A30584; MUID:89176242; PMID:2784458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-268 < YOU>
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
cod Grom of interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
C; Superfamily: interleukin-l
C; Superfamily: interleukin-l
C; Styortokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
P;117-268/Product: interleukin-l beta #status predicted < ILB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA

A,Residues: 1-268 ccAn.>

A,Residues: 1-268 ccAn.>

A,Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633

R,Young, P.R.; Sylvester, D.

R,Young, P.R.; Sylvester, D.

R,Young, P.R.; Sylvester, D.

A,Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and

A,Reference number: A94230; MUID:89315718; PMID:2787507
                                                                                                                                    the right arm of chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPE-----IFFALASSLSSASAEKGSPIL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Gaps
A, Residues: 1-404 <BUS>
A, Residues: 1-404 <BUS>
A, Cross-references: EMBL:236074; NID:9536582; PID:9536583; MIPS:YBR205w
A, Cross-references: EMBL:236074; NID:9536582; PID:9536583; MIPS:YBR205w
R;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
Yeast 9, 797-806, 1993
A,71161e: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of A;Reference number: S34925; MUID:93377417; PMID:8368014
A;Reference number: S4925; MUID:93377417; PMID:8368014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 22.8%; Pred. No. 1.1;
36; Conservative 20; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSF---QP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 RH------VEDRFNNRYHYDWVFLNDQP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2R
C;Keywords: transmembrane protein
F;22-45/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: SGD:S0000409; MIPS:YBR205w
                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z21487
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 22.8*
Matches 36; Conservative
                                                                                                                                                                                                                                                                                A; Residues: 91-352 <BU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-268 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A30584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          렶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
```

THIS PAGE BLAMK (USPIO)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

using sw model - protein search, OM protein

September 29, 2005, 11:03:38 ; Search time 107 Seconds (without alignments) 1043.302 Million cell updates/sec Run on:

US-10-695-195-4

Title: Perfect score:

1 MSFVGENSGVKMGSEDWEKD.....IEFSFQPVCKAEMSPSEVSD 218 Sequence:

Scoring table:

1612378 segs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		рошо	homo	homo	рошо	homo	homo	_	_		-	-		рошо	mus	mus	Q8cga1 mus musculu	-		_	_	-		-	omou.			_		-		Q8axv9 carassius a
SUMMARIES	ΩI		11F7_HUMAN	Q7RU00	Q7RTZ7	11F9_HUMAN	Q7RTZ9	11F6 HUMAN	Q7RTZ8	I1F8_MOUSE	Q6UVX7	11F5_MOUSE	11F9 MOUSE	I1F5_HUMAN	Q7RTZ6	I1F6_MOUSE	I1FA_MOUSE	Q8CGA1	IL1X_MOUSE	I1FA_HUMAN	Q7RTZ5	IL1X_BOVIN	IL1X_RABIT	IL1X_TURTR	073909	Q7RTZ4	IL1X_HUMAN	IL1X_CANFA	Q866 <u>R</u> 8	IL1X PIG	Q9DD <u>F</u> 2	IL1X_RAT	Q8AXV9
	BB	}	н	~	~	-	~	Н	~	-	~	ч	-	ч	~	Н	-	~	-+	н	~	4	ч	-	7	7	-	н	~	н	~		N
	* Query Match Length		218	219	157	169	169	158	158	183	134	156	164	155	155	160	152	159	178	152	.152	174	177	177	267	159	177	176	177	177	272	178	272
	Query Match		1.66	94.5	19.7	19.4	19.4	17.9	17.9	17.9	16.3	•	15.0	14.8	14.8	14.7	14.2	13.8	13.6	13.4	13.4	13.0	12.9	12.9	12.9	12.8	12.8	12.8	12.7	12.6	12.5	12.4	12.2
	000	3 1	1154	1100.5	229	225.5	225.5	209	209	209	190	189.5	174.5	172.5	172.5	171	165.5	191	159	156.5	156.5	152	150.5	150	150	149.5	149.5	149	148	146.5	145.5	144.5	142.5
	Result		1	2	m	4	S	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q71056 brachydanio 018999 equus cabal 071218 carassius a 099gd1 oncorhynchu 08uuq3 oncorhynchu 09dd13 cyprinus ca 05798 cyprinus ca 05798 cyprinus ca 05798 cyprinus ca 05pw18 cyprinus ca 05pw13 sus scrofa P21621 ovis aries 029082 sus scrofa
Q7T056 ILLX HORSE Q712J8 Q712J8 QBUDG3 Q9DDF3 Q9DW18 Q6FW18 Q6FW18 Q6FW18 Q6FW13 ILLB SHEEP Q29082 ILLB SHEEP
000000000000
273 177 177 260 260 276 276 276 28 82 82 264 267
112.11.17.17.17.17.17.17.17.17.17.17.17.17.
140.5 137.5 136.136 136 136 135 128.5 127.5 127.5 127.5
₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩

## ALIGNMENTS

```
SECURNCE FROM N.A. (ISOFORMS B AND C), SEQUENCE OF 46-54, AND VARIANTS VAL-31 AND ALA-42.

MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvarcoff E.,
Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
DETT HUMAN STANDARD; PRT; 218 AA.

GONZH6; QSTD04; QSTD05; Q9HBF2; Q9HBF3; Q9UAA6;
28-FEB-2003 (Rel. 41, Carated)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 7 precursor (IL-IF7) (Interleukin-1 zeta) (Interleukin-1 homolog 4) (IL-1 zeta) (Interleukin-1 related protein) (IL-1 Repl) (IL-1H4)
(Interleukin-1-related protein) (IL-1RP1) (IL-1RP1)
Name=ILIF7; Synonyma=FILLZ, ILIH4, ILIRP1;
                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM B).
TISSUB-Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;
TISSUB-20209405; Pubmed=101044718; DOI=10.1074/jbc.275.14.10308;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzinas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                    Homo sapiens (Human).
Sukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [6]
SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ALA-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECURNCE FROM N.A. (ISOFORMS D AND E).
MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
TAPJOR S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
"Genomic organization of the interleukin-1 locus.";
Genomics 79:726-733(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM B).
TISSUB=Colon carcinoma;
Manoj P.P., Mantovani A., Muzio M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Four new members expand the IL-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1Rrp.";
Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                 Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sims J.E.;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration the tween the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Alausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M. J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garrian A.M., Gay L.J., Hulyk S.W., Whilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketreman M., Madan A., Rodriques S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mutting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska W., Sanchez A., Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.; Toden Ender E.D., Dickson M.C., Schmerzh A., Schein J.E., Jones S.J.M., Marra M.A.; Toden Ender Ende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=Q9NZH6-5; Sequence=VSP_002655; IsSSUE SPECIFICITY: Isoforms A, B and C are expressed in testis, colon, placenta, lung and lymph node. Isoforms D and B were found only in testis and bone marrow. Whereas only isoform A is found in brain, only isoform B in Kidney and only isoform C in heart. INDUCTION: By phorbol ester (PWA) in different cell lines. SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Binds to interleukin-18 receptor (IL-18R) receptor but not to IL-1 receptor. Could be a new player in the inflammatory and immune responses mediated by the IL-18/IL-18R axis.

-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 605510; -. Gextracellular; TAS. GO; 60:0005576; C:extracellular; TAS. GO; GO:0005149; F:interleukin-1 receptor binding; NAS. GO; GO:000555; P:immune reaponse; NAS. InterPro; IPR008996; Cytok IL1 like. InterPro; IPR000975; InterTeukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9NZH6-4; Sequence=VSP_002654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9NZH6-2; Sequence=VSP_002653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9NZH6-3; Sequence=VSP_002656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9NZH6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG14421.1; -. AAF25212.1; -. AAL67151.1; -. AAL67154.1; -. AAH20637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF200496; AAF69252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF167368; AAG29344.1; -. EMBL; AF251118; AAG14420.1; -. EMBL; AF251120; AAG14422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00264; INTERLEUKINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ille.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-InvDB; HIX0002387; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:15563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF251119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF201832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY071840;
EMBL; AY071841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC020637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=D;
```

```
SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                              Removed in mature form.
Interleukin 1 family member 7.
MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLP
                                                                                                                                                                                       Missing (In isoform E).
/FIId=VSP_002655.
SPKVKOLINPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPE
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSFVGENSCVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTWNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of the interleukin-1 gene cluster: construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20545512; PubMed=11093146; DOI=10.1002/1521-4141(200011)30:11
DOI=10.1002/1521-4141(200011)30:11
Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1x, IL-1x and IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                 DPAGSPLEPGPSLPTMNFVHTS -> G (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         IMNFVHTS -> MSGCDRRETETKGKNSFKKRLRG
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654; Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.;
                                                                                                                                                                                                                                                                                                                                        99.1%; Score 1154; DB 1; Length 218; 99.1%; Pred. No. 6.2e-95; ive 0; Mismatches 2; Indels C
/FTId=VAR_014261.
96E089310D2CEA68_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ol-mak-2004 (TrEMBLrel. 26, Created)
Ol-Mak-2004 (TrEMBLrel. 26, Last sequence update)
IL-H7D (IL-IH4, IL-IH, IL-IRPl).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
                                                                                                                                                                                                                               -> K (in isoform /FTId=VSP_002656.
                                                                                                                                                                                                                                                          G -> V. /FIId=VAR_014260.
                                                                                                                                    002653
                                                                                                                                                                            /FTId=VSP 002654
                                                                                                                      isoform A)./FTId=VSP_(
                                                                                                                                                                                                                                                                                        - - A
                                                                                                                                                                                                                                                                                                                 24126 MW;
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                     42
                                                                                                                                                  49
                                                                                                                                                                                          88
                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                  28
                                                                                                                                                                                          28
                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                        Best Local Simi
Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7RU00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

ö

```
SEQUENCE FROM N.A.
MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J.,
Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
"Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cytc.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yangura D., Lewis L., Bigenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kastelein R.A.; "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
integrated YAC/PAC contig and a partial transcriptional map in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20118623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=94245215; PubMed=8188271;
Nicklin M.J.H., Weith A., Duff G.W.;
"A physical map of the region encompassing the human interleukin-1-
alpha, interleukin-1-beta and interleukin-1 receptor genes.";
Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young P.R.; and initial characterization of four novel members
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A sequence-based map of the nine genes of the human interleukin-1 cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
MEDLINE-20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
Kumar S., McDonnell B.C., Lehr R., Tierney L., Trimas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; MEDLINE=99443727; Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.; arillHY1: A novel interleukin-1 receptor antagonist gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21359532; PubMed=11466363; Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Four new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e interleukin-1 family.";
Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 276:20597-20602(2001).
                                   region of chromosome 2q13.";
Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 79:718-725(2002).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1Rrp.";
Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sime
          REPARA PARTER PA
```

```
SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; Sims S.T., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J., Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G., Pan Y., Smith D.E., Young P.R.; A new nomenclature for the IL-1-family genes."; Trends Immunol. 22:536-537(2001).

-I MISCELLANEOUS: The sequence shown here is derived from an ENBL/GenBank/DDBJ third party annotation (TPA) entry.

-I SINILARITY: Belongs to the IL-1 family.

HSSP; QQQYI; IMD6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAVSPLEPGPSLPAMNFVHTSPKVKNLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASABKGSLILLGVSKGEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=20545212; PubMed=11093146; DOI=10.10621529::AID-IMMU3299>3.0.CO;2-S; DOI=10.1002/1521-4141(200011)30:11<-3299::AID-IMMU3299>3.0.CO;2-S; Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.; A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."; Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:000576; C:extracellular; IEA.
GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.
GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97312631; PubMed=9169134; DOI=10.1006/geno.1997.4654;
Nothwang H.G., Schahm B., Denich D., Kuebler M., Schwabe J.,
Nothwang H.G., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,
1 receptor-related protein 2.J. Immunol. 167: 1440-1446."; Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1100.5; DB 2; Length
Pred. No. 3.7e-90;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0264; INTERLEUKIN1.
PRINTS; PRO1360; INTELEUKIN1.
1; 1.
PRODOM; PD002536; Interleukin 1; 1.
SEQUENCE 219 AA; 24242 MW; 18EBA0881DF25C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNCNEPVGVTDKFENRKHIEFSFQP-VCKAEMSPSEVSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008996; Cytok II. like.
InterPro; IPR003297; Interleukinil. IPA.
InterPro; IPR000975; Interleukin. 1.
Pfam: PF00340; III.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.3
Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00340; IL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL-1F8 (FIL1-eta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O7RTZ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SO DE REPRETATA DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

ä

09

120

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200; Lin H.S., Ho A.S., Halbey-Vicente D., Zhang J., Bernal-Fussel J., Pace A.M., Hansen D., Schweighofeer K., Mize N.K., Ford J.E.; "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.,
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                     "Molecular cloning of the interleukin-1 gene cluster: construction of
an integrated YAC/PAC contig and a partial transcriptional map in the
region of chromosome 2q13";
Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Identification and initial characterization of four novel members of
                                                                                                                                                                          MEDLINE=94245215; PubMed=8188271; Nicklin M.J.H., Weith A., Duff G.W.; "A Physical map of the region encompassing the human interleukin-1-alpha, interleukin-1-beta and interleukin-1 receptor genes."; Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                             "A sequence-based map of the nine genes of the human interleukin-1 cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BUBLINES-2018623, PubMed=10860666; DOI=10.1006/geno.2000.6184;
Busfixeld S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
Identification and gene organization of three novel members of th
II-1 family on human chromosome 2.";
Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; Mulero J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.; Ford J.E.; IlliHY1: A novel interleukin-1 receptor antagonist gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21359532; PubMed=11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Four new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : interleukin-1 family.";
Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ber.";
Biol. Chem. 276:20597-20602(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 79:718-725(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sime J.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1Rrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
  BARKERITTER RETTTER RETTTTER RETTTTER RETTTER RETTTTER RETTTTER RETTTTER RETTTTER RETTTTER
```

```
RN (12)

SEQUENCE FROM N.A.

The J. Immunol. 16/:1440-14480(2001).

RN SEQUENCE FROM N.A.

MEDINES—145916; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; Pan Stan Sima J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J., Rastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G., Pan J.E., Micklin M.J., Bazan J.F., Barton J.L., Busfield S.J., Rastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G., RA Pan Y., Smith D.E., Young P.R.;

RA Pan Y., Smith D.E., Young P.R.;

Trends Immunol. 22:536-537(2001).

C. - MISCELLANEXOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.

C. - SIMILARITY: Belongs to the IL-1 family.

EMBL/GenBank/DDBJ third party annotation (TPA) entry.

C. - SIMILARITY: Belongs to the IL-1 family.

DR RASP; O90YY1: 1MD6.

C. - SIMILARITY: PROJOS976; C:extracellular; IEA.

BR GO; GO:00065149; F:interleukin-1 receptor binding; IEA.

GO; GO:00065149; F:interleukin-1 RA.

BR GO; GO:00065149; F:interleukin-1 RA.

BR GO; GO:00065149; F:interleukin-1 RA.

BR THEOFYO; IPRO0349; ILI 1: 1.

BR FRINTS; PROJOS94; Interleukin-1 RA.

BR FRINTS; PROJOS94; INTELEUKINIB.

BR FRINTS; PROJOS95; INTELEUKINIB.

BR PRINTS; PROJOS95; INTERLEUKINIB.

BR PRINTS; PROJOS95; INTERLEUKINIB.

BR PRINTS; PROJOS95; INTERLEUKINIB.

BR PRODOM; PDOJOS536; INTERLEUKINI-1; 1.

BR PRODOM; PROJOSS3; INTERLEUKINI-1; 1.

BR PRODOM; PROJOSS3; INTERLEUKINI-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALA-SSLSSASAEKGSPILLGVSK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 PKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIKG 68
"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446."; J. Immunol. 167: 1440-1446 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young P.R.; "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ....ezieukin 1 family member 9 (IL-1F9) (Interleukin-1 homolog 1) (IL-1H1) (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1RP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Keratinocytes;
MEDLINES-27094615; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.7%; Score 229; DB 2; 34.8%; Pred. No. 1.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
26-UUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 9 (IL-1F9) (Inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IL1F9; Synonyms=IL1E, IL1H1, IL1RP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FICTSCNCNEPVGVT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || || :|: :|
126 FIATSTTSGQPIFLT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 34.8 ses 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 11F9 | HUMAN | 11F9 | HUMAN | 11F9 | HUMAN | 128 - FEB | DT | 05 - UTL | DE | 11 | (15 - UTL | 12 | HUMAN | 13 | HUMAN | 13 | HUMAN | 14 | HUMAN |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9NZH8
```

m ,

വ

```
180 SCNCNEPVGVTDK 192
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sime J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cluster."
                                                                                                                                                                                                                                                                        Q7RTZ9
                                                                                                                                                                                                                                                                                                            RAPARA RA
                                                                        셤
        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-EROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=2018623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
MEDLINE=2018623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
A Busfield S.J., Conrack C.Z., Yu G., Chickering T.W., Smutko J.S.,
Busfield S.J., Conrack C.Z., Yu G., Chickering T.W., Smutko J.S.,
A zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pau Y.;
IL-1 family on human chromosome 2.";
Genomics 66:213-216(2000).
Genomics 66:213-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAE-KGSPILLGVSKGEFC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 TINDLNQQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                Kastelein R.A.;
"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, funct
as an antagonist and agonist of NF-kappa B activation through the
orphan IL-1 receptor-related protein 2.";
J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                    :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes. SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                        Sana T.R., Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:000267; P:cell-cell signaling; TAS.
GO; GO:0009613; P:response to pest/pathogen/parasite; TAS.
InterPro; IPR008996; Cyrok ILI_like.
InterPro; IPR009975; InterTeukin_1.
Pfam; PP00340; ILI; 1.
                                                                                                                                                                TISSUB=Epithelium;
MEDLINB=21359532;
DubMed=11466363;
Debete R., Timans J.C., Homey B., Zurawski S., Sana T.R.,
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Multigene family.
SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.4%; Score 225.5; DB 38.3%; Pred. No. 4e-12; tive 26; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00125; IL1; 1.
PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION.
            s interleukin-1 family.";
Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00264; INTERLEUKINI.
ProDom; PD002536; Interleukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP200492; AAF69248.1; -. EMBL; AP206696; AAG35670.1; -. HSSP; P18510; 11LR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:15741; IL1F9.
MIM; 605542; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

ઠે

```
"Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13.";
Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young P.R.; "Identification and initial characterization of four novel members of the interleukin-1 family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.; "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."; Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=94245215; PubMed=8188271;
Nicklin M.-U., Weith A., Duff G.W.;
Nicklin map of the region encompassing the human interleukin-1-
alpha, interleukin-1-beta and interleukin-1 receptor genes.";
Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

BEDLINES-20203405; Pubmed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20545212; Pubmed=11093146;
DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; Mulero J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.; "ILLIHY1: A novel interleukin-1 receptor antagonist gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE TO 1074/jbc.275.2.1169; MEDITURE 20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "ILLHY1: A novel interleukin-1 receptor antagonist gene.";
Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Four new members expand the interleukin-1 superfamily.";
                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 169 AA.
                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Last annor.
IL-189 (IL-111, IL-1RP2, IL-1-epsilon)
Name=IL1F9;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 79:718-725(2002).
| ::|::|:
143 S-KRDQPIILTSE 154
```

```
셤
                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAE-KGSPILLGVSKGEFC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 LYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sime J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,
Sime J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,
A Port J.E., Kastellein R.J., Kumar S., Lin H., Mulero J.J., Pan G.,
Pan Y., Smith D.E., Young P.R.,
Trands Immunol. 22:354-537(2001).
Trands Immunol. 22:354-537(2001).
Trands Immunol. 22:355-373(2001).
Trands Immunol. 22:355-373(2001).
Trands Immunol. 22:355-373(2001).
Trands Immunol. 25:365-373(2001).
Trands Immunol. 25:37(2001).
Trands Immunol. 25:37(2001).
Trands Immunol. 25:37(2001).
The Second Interpretation of TPA) entry.
The Second Interpretation of TPA and an antagonist activity; IEA.
The Prop. IPR00895; Filmunual response; IEA.
The Prop. IPR00895; Pilmunual response; IEA.
The Prop. IPR00895; Interleukin_1.
The Prop. IPR00895; Interleukin_1.
The Prop. IPR00895; Interleukin_1.
                                                                                                                                                                                                                                                                                           MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J.,
Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
"Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                     MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cytc.2000.0799; Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E., Yangura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.; "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446."; J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 TINDINQOVWTLOGONLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIONPEMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                           SEQUENCE FROM N.A. MEDIALIZE=20111006/geno.2000.6184; MEDIZIRE=20118623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Bubfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                        S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.4%; Score 225.5; DB 2; Length 169; 38.3%; Pred. No. 4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21359532; PubMed=11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO0264; INTERLEUKINI.
PRO1360; INTERLEUKINIX.
PRO1366; INTERLEUKINIX.
PD002536; INTERLEUKINI.1 1.
E 169 AA; 18721 MW; F00A9243706F4154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Mismatches
                                                                                                                                                                                                                                                                                                                                                               ber.";
Biol. Chem. 276:20597-20602(2001)
Biol. Chem. 275:10308-10314(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 SCNCNEPVGVTDK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Conservative
                                                                                                                                                                                                                                               Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 PKKFSIHDQDHKVLVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 KGEFCLYCDKDKGOSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANBOUS: Binding analysis failed to detect interaction with multiple ILIR family members.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 6 (IL-1F6) (Interleukin-1 epsilon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17684 MW; 469AC84306B0E280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO. GO: 0005576; C:extracellular; NAS. GO: 0005149; F:interleukin-1 receptor binding; NAS. GO: 0005149; F:interleukin-1 receptor binding; NAS. GO: 0006955; P:immune response; NAS. InterPro; IPR000996; Cytok IL1 like. InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.9%; Score 209; DB 1; 36.7%; Pred. No. 1.1e-10; ive 26; Mismatches 61
                                                                                                                                                                     158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIMIT, FROOZ64; INTERLEUKINI.
PRODOM; PROO2536; INTERLEUKIN_1; 1.
SMART; SM00125; ILI; 1.
PROSITE; PSO0253; INTERLEUKIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WFICTSCNCNEPVGVTDKFENRKHIEF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 WFIAVSSEGGCPLILTQELGKANTTDF 152
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                            Name=IL1F6; Synonyms=FIL1E, IL1E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF201831; AAF25211.1; -.
HSSP; P01584; 1L2H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine, Multigene family.
| ::|::|:
143 S-KRDQPILLTSE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:15562; IL1F6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Conservative
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                       epsilon) (FIL1 epsilon)
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sims J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                     IIF6 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

4

```
1Rrp.";
SO DER DER DER DER DE PRESENTATION DE PRESENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13.";
Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20545212; PubMed=11093146;
DOI=10.1002/1521-4141(200011)30:11<2399::AID-IMMU3289>3.0.CO;2-S;
Barton J.L., Herbst R., Boalsho D., Higgins L., Nicklin M.J.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-11a, IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94245215; PubMed=8188271;
Nicklin M.J.H., Weith A., Duff G.W.;
"A Physical map of the region encompassing the human interleukin-1-
alpha, interleukin-1-beta and interleukin-1 receptor genes.";
Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification and initial characterization of four novel members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [5]
SEQUENCE FROM N.A.
MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
Mulero J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R.,
Drmanac R., Ford J.E.;
"ILIHY1: A novel interleukin.1 receptor antagonist gene.";
Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDIATOR DOI=10.1006/geno.1997.4654; MEDIATURE 97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654; Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Nothwang H.G., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.;
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                      158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-1 family.";
Biol. Chem. 275:10308-10314(2000).
                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 275:1169-1175(2000).
                                                                                                                           (TrEMBLrel. 26, (TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 79:718-725(2002).
                                                                                        PRELIMINARY;
                                                                                                                                                                                           IL-1F6 (FIL-1-epsilon)
                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                               01-MAR-2004
01-MAR-2004 (
                                                                                                                                01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                foung P.R.;
                                                                                                                                                                                                                 Name=IL1F6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cluster.
                                                                                   Q7RTZ8
                                                                                                            Q7RTZ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
```

```
WEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; SEQUENCE FROM N.A.

MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; A SIME J.B., Nacklin M.J., Bazan J.F., Barton J.L., Busfield S.J., A SHE J.B., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G., A Ford J.B., Xanth D.E., Young P.R.; A new nomenclature for the IL-1-family genes."; Trends Immunol. 22:536-537(2001).

Trends Immunol. 22:536-537(2001).

Trends Immunol. 22:536-573(2001).

T. SIMILANITY: Bablongs to the IL-1 family.

C. -1- SIMILANITY: Bablongs to the IL-1 family.

EMBL, GAD20002; CAD29875.1; --.

BR GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0006576; P:inmune response; IEA.

BR GO; GO:0006955; P:immune response; IEA.

BR GO; GO:0006956; P:immune response; IEA.

BR GO; GO:0006956; P:immune response; IEA.

BR InterPro; IPR003294; InterleukinILIB.

BR InterPro; IPR003296; IRR003296; INTERLEUKINILAB.

BR INTERPRO; IPR003296; INTERLEUKINILAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J.,
Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
"Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21066552; PubMed-11145836; DOI=10.1006/cyto.2000.0799;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21359512; PubMed=11466363;
Debete R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo
Magner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0264; INTERLEUKINI.
PRINTS; PR01359; INTRLEUKINIB.
PRINTS; PR01357; INTELEUKINIB.
ProDom; PD002536; Interleukin 1; 1.
SEQUENCE 158 AA; 17684 MW; 469AC84106B0E280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.9%; Score 209; DB 2; 36.7%; Pred. No. 1.1e-10; iive 26; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 WFICTSCNCNEPVGVTDKFENRKHIEF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ber.";
Biol. Chem. 276:20597-20602(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00340; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 54; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
```

4

SEQUENCE FROM N.A.

```
REAL STRAINGSTEE TONGUE;

REAL MEDINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

REAL MEDINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

REAL STRAINGSTEE, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Swiss Webster / NIH;
MEDLINE=2198851; PubMed=11991723; DOI=10.1006/geno.2002.6752;
Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.B.;
"Genomic organization of the interleukin-1 locus.";
Genomics 79:726-733(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 420:563-573(2002).
-1- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                        Q9D6Z6; Q8R461;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 8 (IL-1F8).
                                                                                                                                                        183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the IL-1 family.
| | | | | : | : | : | 126 WFIAVSSEGGCPLILTQELGKANTTDF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY071842; AAL67152.1; ALT_INIT.
EMBL; AK009787; BAB26505.1; -.
                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01584; 1L2H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                     IIF8 MOUSE
                                                                                                     RESULT 8
                                                                                                                                                                                윰
```

InterPro, IPR008996; Cytok\_IL1\_like

MGD; MGI:1916927; Illf8.

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 TAVPASNINVKPVILSILACRDTEFQDVKKGNLVFLGIKNRNLCFCCVEMEGK--PTLQLK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The secreted protein discovery initiative (SPDI), a large-scale of effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

"The sassessment.";

"Genome Res. 13:2265-2270(2003).

"C -1- SIMILARITY: Belongs to the IL-1 family.

"BMBL, ANSS9111, AAQ89469.1;

"R GO; GO:0005576; C:extracellular; IEA.

"R GO; GO:0005576; P:interleukin-1 receptor antagonist activity; IEA.

"R GO; GO:0005576; P:interleukin-1 receptor antagonist activity; IEA.

"R GO; GO:0005576; P:interleukin-1 ike.

"R InterPro; IPR008996; Cytok IL1 like.

"R InterPro; IPR000975; Interleukin-1.

"R PRINTS; PR00264; INTERLEUKINIA.

"R PRINTS; PR01360; INTRLEUKINIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PQSCVH-----VLPPKSIQMWEPNHNTMHGSSQ----SPRNYRVHDSQQMVWVLJGNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 IAVPDKNYIRPEIFFALA-SSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 POCCLEDPAVSPLEPGPSL----PAMNFVHTSPKVKNLNPKKFSIHDQDHKVLVLDSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-2289726; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE-2289726; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE-2289726; PubMed=12975309; DOI=10.1101/gr.1293003; Chark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Douel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Van G., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                Query Match 17.9%; Score 209; DB 1; Length 183; Best Local Similarity 31.1%; Pred. No. 1.3e-10; Matches 51; Conservative 32; Mismatches 63; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 KEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.3%; Score 190; DB 2; Length 13 ilarity 45.5%; Pred. No. 4.4e-09; Conservative 17; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; ILL; 1.
SEQUENCE 134 AA; 14928 MW; D5369C5AD44A9752 CRC64;
                                                                                                                                       SMART; SM00125; ILL; 1.
PROSITE; PS00233; INTERLEUKIN_1; 1.
Cytokine; Multigene family.
SEQUENCE 183 AA; 20878 MW; A3ACB339FB96F02F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
InterPro; IPR000975; Interleukin_1.
                                                Fram; Frudstv; 111; 1.
PRINTS; PR00264; INTERLEUKINI.
ProDom; PD002536; Interleukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                     Pfam; PF00340; IL1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=UNQ2456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6UVX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDT TABLE TO THE TOTAL TO THE TOTAL TO THE TABLE TABLE TABLE TO THE TABLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
SOLUTION DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DE LA PRESENTA DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DEL PRESENTA DE LA PRESENTA DE LA PRESENTA DE LA PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB=Stomach, and Tongue;

STRAIN-C57BL/6J; TISSUB=Stomach, and Tongue;

MEDINRE-2534683; PubMed=12466851; DOI=10.1038/nature01266;

Nakaido I., Osato N., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Naja K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hothia C., Corbani D.B., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani D.B., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani D.B., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani D.B., Cousins S.,

Canala E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,

Crimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Konagaya A., Kurochkin I.V., Lee Y., Lehard B.J., Lyons B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lehard B.J., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
KGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSW 164
                           "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 47, Last Sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1
delta) (Interleukin-1-like protein-1) (Interleukin-1-like protein 1)
(IL-1L1) (Interleukin-1 HY1) (IL-1HY1) (Interleukin-1 homolog 3) (IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20545512; PubMed=11093146; DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S; DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S; Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.H.; A rissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."; Bur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21359532; PubMed=11466363; MEDLINE=21359532; PubMed=11466363; Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                               156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Illf5; Synonyms=Filld, Illh3, Illhy1;
                                                                                                                                        NMLESAAHPGWFICTSCNCNEPVGVTDK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                               11F5 MOUSE STANDARD;
Q9QYY1; Q9JIG2;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner J., Edwa
Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young P.R.;
                                                                                                            165
     105
                                                                                                                                                            93
                                                                                                                                                                                                                                                                            I1F5_MOUSE
                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1H3)
                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                               ઠ
                                                                                                                                                               g
```

```
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Vinning L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninol P., Hayateu N.,

R. Hirozane-Kishikawa T., Konno H., Nakawura M., Sakazuen N., Sakatuen N., Sazu K.,

R. Haraki T., Waki K., Kawai J., Alzawa K., Arakwa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Miyazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RA Birney E., Hayashizaki Y.;

RA Birney E., Hayashizaki Y.;

Raunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

Raunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

R. Manalysis of the mouse transcriptome based on functional annotation of the Incompany of Incompany of the Incompany of Incompany Incompany of Incompany 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 FSIHDODHKVLVLDSGNLIA--VPDKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 FCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGSWNMLESAAHPGWF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 FRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEEISVVPNRALDASL---SPVILGVQGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 2 Missing (in Ref. 3).
156 AA; 17136 MW; A4D1EE2F93CF77A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%; Score 189.5; DB 1
37.3%; Pred. No. 5.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00253; INTERLEUKIN 1; 1.
3D-structure, Cytokine, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ250429; CAB59831.1; ALT_INIT. EMBL; AF200495; AAF69251.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR008996; Cytok III like.
Interpro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00340; IL1; 1.
PRINTS; PR00264; INTERLEUKIN1.
PRODOM; PD002536; INTERLEUKIN1.; 1.
SMART; SM00125; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF230378; AAF91275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK009741; BAB26471.1; -. EMBL; AK008977; BAB26002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 ICTSCNCNEPVGVT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||| ::|| :|
LCTSPEADQPVRLT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1MD6; X-ray; A=3-156.
MGD; MGI:1859325; Illf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIF9 MOUSE
ID IIF9 MOUSE
AC Q8R460;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
```

```
Name=IL1F5; Synonyms=FIL1D, IL1HY1, IL1L1, IL1RP3;
             Homo sapiens
                                                                                                     Sims J.E.;
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 IHDODHKVLVLDSGNLIAVPDKNYIRPEIFFALASSL-SSASAEKGSPILLGVSKGEFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 VFDLDQQVWIPRNQALVTVPRSHRVTPVSVTILPCKYPESLEQDKGIAIYLGIQNPDKCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .21 YCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 44, Last annotation update)
65-UUJ-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 5 (IL-IF5) (Interleukin-1 delta) (IL-1
delta) (FILI delta) (Interleukin-1-like protein 1) (IL-ILI)
(Interleukin-1 HY1) (IL-IHY1) (Interleukin-1 receptor antagonist homolog 1) (IL-Ira homolog 1) (IL-IRB3)
                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 174.5; DB 1; Length 164; 31.7%; Pred. No. 1.4e-07; ive 26; Mismatches 66; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine; Multigene family. SEQUENCE 164 AA; 18733 MW; A7338D475DFEADBE CRC64;
  05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
           Interleukin 1 family member 9 (IL-1F9)
                                                                                                                                                                                                                                                                                                                                           MMD; MGI:2449929; II11f9.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR000975; InterTeukIn_1.
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00264; INTERLEUKINI.
ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CNCNEPVGVTDKFENRKHIEFS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 KTGN-PIFLTSKKGEYYNINFN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                          EMBL; AY071843; AAL67153.1; -. HSSP; P01584; 1L2H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00340; IL1; 1.
                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homolog 1) (IL-1ra
(UNQ1896/PRO4342)
                                                                                   SEQUENCE FROM N.A.
                                                              NCBI_TaxID=10090;
                     Name=Illf9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIFS HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHEU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIFS HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
DOI=10.1002/1521-4141(200011)30:11<2299::AID-IMMU3299>3.0.CO;2-S;
Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.H.;
"A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22887296; PubMed=12975109; DOI=10.1101/gr.1293003;
Clark H.F., durney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
Clark H.F., durney A.L., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Roster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDINEGE1086066; DOI=10.1006/geno.2000.6184; MEDILINE=2018623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, funct as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2.";
Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :
:
                                                                                                                                                                                                                                                                  MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal skin;
MEDLINE=9944377; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
MALDETO J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
Drmanac R., Ford J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21359532; PubMed-11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F., Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "ILIHY1: a novel interleukin-1 receptor antagonist gene.";
Biochem. Biophys. Res. Commun. 263:702-706(1999).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                              "Four new members expand the IL-1 superfamily.";
J. Biol. Chem. 275:1169-1175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL-1 family on human_chromosome 2.";
Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20545212; PubMed=11093146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=Placenta;
                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                             TISSUE=Placenta;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106
                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U. S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U. S.A. 99:16899-16903(2002).

- -- FUNCTION: Is a highly and a specific antagonist of the IL-1 receptor-related protein 2-mediated response to interleukin. I family member 9 (ILIP9). Could constitute part of an independent signaling system analogous to interleukin-1 alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-1B). that is present in epithelial barriers and takes part in local inflammatory response.

--- SUBCELLULAR IOCATION: Secreted.

--- TISSUE SPECTIFICITY: Predominantly expressed in keratinocytes but not in fibroblasts, endothelial cells or melanocytes. Detected also in the spleen, brain leukocyte and macrophage cell types.

--- Increased in lesional psoriasis skin.

--- INDUCTION: By phorbol ester (PRA) and lypopolysaccharide (IPS)

--- SIMILARITY: Belongs to the IL-1 family.
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McErnan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lux , Gibbs R.A., Palekon E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 FRMKDSALKVLYLHNNQL------LAGGLHAGKVIKGEEISVVPNRWLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 605507; -.
GO; GO:0005152; F:interleukin-1 receptor antagonist activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 FSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine; Multigene family. SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 172.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00996; Cytok III like.
InterPro; IPR00975; InterTeukIn_1.
Pfam; PP0040; III, 1.
PRINTS; PR00264; INTERLEUKINI.
ProDom; PD002536; InterTeukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00125; IL1; 1.
PROSITE; PS00253; INTERLEUKIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF201830, AAF25210.1; --
EMBL, AF186094; AAF02757.1; --
EMBL, AJ242734; CAB59822.1; --
EMBL, AJ242738; CAB59823.1; --
EMBL, AJ271338; CAB5704.1; --
EMBL, AF230377; AAF91274.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY359117; AAR91274.1; -. AY359117; AAQ89475.1; -. BC024747; AAH24747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.6%;
                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P18510; IILR.
Genew; HGNC:15561; IL1F5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JC7104; JC7104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

107 --SPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS 163

<u>:</u> :: ::

ઠે

```
53 SLSPVILGVQGGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13."; Genomics 41:370-378(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young P.R.; "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20545212; PubMed=11093146;
DOI=10.1002/1521-4141(200011)30:11<2299::AID-IMMU3299>3.0.CO;2-S;
DOI=10.1002/1521-4141(200011)30:11<2299::AID-IMMU3299>3.0.CO;2-S;
Barton J.L., Herbet R., Bosisio D., Higgins L., Nicklin M.J.;
Barton J.L., Aissue specific II-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
Eur. J. Immunol. 30:3299-3308(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicklin M.J.H., Weith A., Duff G.W.; "A Physical map of the region encompassing the human interleukin-1-alpha, interleukin-1-beta and interleukin-1 receptor genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE-20209465; Pubmed-10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A sequence-based map of the nine genes of the human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440; Mulero J.J., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.; "ILIHY1: A novel interleukin-1 receptor antagonist gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97312693; PubMed-9169134; DOI=10.1006/geno.1997.4654; Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ILLHY1: A novel interleukin-1 receptor antagonist gene.";
Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Created)
U-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
IL-1F5 (IL-1HYI, FIL1-delta, IL-1RP3, IL-1L1, IL-1-delta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Four new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94245215; PubMed=8188271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 79:718-725(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 19:382-384(1994).
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kornman K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sime J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cluster."
                                                                                                                                                                                                                                                                                                                                                                O7RTZ6;
                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                A COOCCOOR SELECT THE SELECT S
                                                                             ò
                                                                                                                                               유
```

```
EXCUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDINIE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Madaika I., Osato N., Bate R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Fadiarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Full D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Kamapin H., Batalov S., Beisel K.W.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kamai H., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kamai H., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kamai T., Namata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Rayasima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Rayasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sultena R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultena R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Hirozane-Kishikawa T., Konno H., Nakawura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawa J., Alazawa K., Arakawa T., Pukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Yasunishi A., Yoshihoo M., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshihoo M., Waterston R., Lander E.S., Rogers J.,
--SPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS 163
                      53 SLSPVILGVQGGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birney B., Hayashizaki Y.; ahnalysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                           C30-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 6 (IL-IF6) (Interleukin-1 epsilon) (IL-1
epsilon) (FIL1 epsilon) (Interleukin-1 homolog 1) (IL-1H1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINES-2009405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kastelein R.A.;
"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, funct
s an antagonist and agonist of NF-kappa B activation through the
orphan IL-1 receptor-related protein 2.";
J. Immunol. 167:1440-1446(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zurawski S., Sana T.R., Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21359532; PubMed=11466363; Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                          : ||||:||||:||
108 TSSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139
                                                                                      164 WNMLESAAHPGWFICTSCNCNEPVGVTDKFEN 195
                                                                                                                                                                                                                                         160 AA.
                                                                                                                                                                                                                                                                                                                                                                        epsilon) (FIL1 epsilon) (Interleukin-1 ho
Name=Illf6; Synonyms=Fille, Ille, Illh1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 family."
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young P.R.;
                                                                                                                                                                                                                                           IIF6 MOUSE
  101
                                                                                                                                                                                                                                                                  g
                                                                                      à
                                                                                                                               g
    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; Sims J.B., Nicklin M.J. Bazan J.F., Barton J.L., Busfield S.J., Pond J.E., Kastelein M.J., Razan J.F., Barton J.L., Busfield S.J., Pand J.E., Xaith D.E., Young P.R., Lin H., Mulero J.J., Pan G., An new nomenclature for the IL-1-family genes."; Trends Immunol. 22:536-537(2001).

Trends Immunol. 22:536-537(2001).

Trends Immunol. 22:536-537(2001).

Trends Immunol. 22:536-537(2001).

SMEJ, BNOGOOGS, The sequence shown here is derived from an EMBL; BNOGOOGS, CAR29897.1; C. I- SIMILARITY: Belongs to the IL-1 family.

EMBL; BNOGOOS, CAR29877.1; C. Extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; P:interleukin-1 receptor antagonist activity; IEA.

GO; GO:0005954; P:inflammatory response; IEA.

RINEEPRO; IPRO08996; Cytok IL1, like.

INTERPO: IPRO0896; Cytok IL1, like.

INTERPO: IPRO03266; Interleukin-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200; Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J., Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.; "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
                                                                                                                                                                                                                                                                MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cytco.2000.0799; Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E., Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.; "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRMKDSALKVLYLHNNQL-------LAGGLHAGKVIKGEEISVVPNRWLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                 MEDITRE-2018623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the Genomics 66:213-216(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 172.5; DB 2; Length 155; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21359532; PubMed=11466363; Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 FSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSSASAEKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003297; InterleukinILIRA.
InterPro; IPR000975; Interleukin_1.
Pfam; PP00340; IL1; 1.
PRINTS; PR00264; INTERLEUKINI.
PRINTS; PR01359; INTRLEUKINIB.
PRINTS; PR01360; INTRLEUKINIB.
ProDom; PD002536; Interleukin_1; 1.
PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN 1.
SEQUENCE 155 AA; 16962 MW; B96DBSERAZ612E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                      Chem. 275:10308-10314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 276:20597-20602(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.6%;
  interleukin-1 family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Cytokine 13:1-7(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                        Biol.
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     member.
                                                                                                                                                                                                                                                                                                                                                          1Rrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
      ઠે
```

function

ŝ

```
셤
                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                       8
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 KVKNINPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFAL-ASSLSSASAEKGSPI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPVTITLLPCQYLDTLETNRGDPT
            Nature 420:563-573(2002).
-!- SUBCELLUIAR LOCATION: Secreted (Potential).
-!- TISSUB SPECIFICITY: Highly expressed in embryonic tissue and in tissues containing epithelial cells.
-!- MISCELLANEOUS: Binding analysis failed to detect interaction with multiple ILIR family members.
-!- SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
9
                                                                                                                                                                                                                                                                                                                                                                                                               Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                           Cytokine, Multigene family. SEQUENCE 160 AA, 18015 MW, AA0434D68FF62F4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               14.7%; Score 171; DB 1; 31.6%; Pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8R459;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin 1 family member 10 (IL-1F10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 AA
                                                                                                                                                                                                                                                                                                                                    ProDom; PD002536; Interleukin_1; 1.
SMART; SM00125; IL1; 1.
PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Mismatches
                                                                                                                                                                                                                 EMBL, AF200493, AAF69249.1; -.
EMBL, AF206697, AAG35671.1; -.
EMBL, AK004061; BAB23147.1; -.
HSSP; POLS84; JHTB.
MGD; MGI:185934; Illf6.
InterPro; IPR008996; Cyrok_ILl like.
InterPro; IPR000995; Interleukin_1.
Pfam; PF00340; ILl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                        PRINTS; PR00264; INTERLEUKINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 AAHPGWFI--CTSCNC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 AAFPGWFIAVCSKGSC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=111f10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIFA MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIFA MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

```
CC This SWISS-PROT entry is copyright. It is produced through a collaboration conclude the Swiss Institute of Bioinformatics and the EMBL outstation to the European Bioinformatics and the EMBL outstation on its conditied and this statement is not removed. Usage by and for commercial contities requires a licenseals as long as its content is in no way contities requires a licenseals beloch.

CC or send an email to licenseals beloch.

CC or send an email to licenseals beloch.

EMBL, AV071844; AAL67155.1; -.

DR HSSP, PRO00349; Interleukin.

DR HORDS PRO00349; Interleukin.

DR PRO00340; Interleukin.

DR PRO00340
```

Search completed: September 29, 2005, 11:16:36 Job time : 107 secs

THIS PAGE BLANK (USPTO)